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OM protein - protein search, using sw model

Run on: March 3, 2004, 12:33:10 ; Search time 15.317 Seconds
(without alignments)
734.770 Million cell updates/sec

Title: US-09-825-561A-6
Perfect score: 1195
Sequence: 1 CPDLVCYTDYLTQVICILEM.....SDPVFQTSBELKEGNPH 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1195	100.0	538	3	US-09-040-005-2
2	1195	100.0	538	4	US-09-522-217-115
3	1195	100.0	538	4	US-09-404-641-2
4	1195	100.0	538	4	US-09-923-246-115
5	1195	100.0	538	4	US-10-295-723-115
6	1195	100.0	606	4	US-09-522-217-97
7	1195	100.0	606	4	US-09-404-641-51
8	1195	100.0	606	4	US-09-923-246-97
9	1195	100.0	606	4	US-10-295-723-97
10	844	70.6	529	4	US-09-404-641-85
11	838	70.1	529	4	US-09-732-234-6
12	838	70.1	529	4	US-08-784-859-6
13	400	33.5	397	4	US-09-404-641-81
14	144	12.1	783	4	US-08-780-562-7
15	144	12.1	894	2	US-08-599-455B-2
16	144	12.1	894	3	US-09-069-781B-2
17	144	12.1	894	4	US-08-618-957A-12
18	144	12.1	894	4	US-09-137-132-2
19	144	12.1	894	4	US-08-864-564A-2
20	144	12.1	894	4	US-09-094-410-2
21	144	12.1	894	4	US-08-708-123D-2
22	144	12.1	894	4	US-08-583-153A-2
23	144	12.1	894	4	US-08-570-142D-2
24	144	12.1	894	4	US-08-638-524B-2
25	144	12.1	1162	2	US-08-593-455B-43
26	144	12.1	1162	3	US-09-063-781B-43
27	144	12.1	1162	4	US-09-137-132-43

28	144	12.1	1162	4	US-08-864-564A-43	Sequence 43, Appl
29	144	12.1	1162	4	US-09-094-410-43	Sequence 43, Appl
30	144	12.1	1162	4	US-08-708-123D-43	Sequence 43, Appl
31	144	12.1	1162	4	US-08-638-524B-43	Sequence 12, Appl
32	142.5	11.9	896	2	US-08-640-389A-12	Sequence 12, Appl
33	141.5	11.8	539	6	5198359-4	Patent No. 5198359
34	141.5	11.8	539	6	5449756-4	Patent No. 5449756
35	140.5	11.8	691	4	US-09-313-942-20	Sequence 20, Appl
36	140.5	11.8	694	4	US-09-313-942-22	Sequence 22, Appl
37	140.5	11.8	784	4	US-09-313-942-30	Sequence 30, Appl
38	139	11.6	493	2	US-08-078-311-7	Sequence 7, Appl
39	139	11.6	493	2	US-08-460-402-7	Sequence 7, Appl
40	139	11.6	635	1	US-08-184-327A-4	Sequence 4, Appl
41	139	11.6	635	2	US-08-078-311-1	Sequence 1, Appl
42	139	11.6	635	2	US-08-460-402-1	Sequence 1, Appl
43	139	11.6	635	5	PCT-US95-00670-4	Sequence 4, Appl
44	138	11.5	895	3	US-08-827-962-19	Sequence 19, Appl
45	138	11.5	1162	3	US-08-827-962-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-09-040-005-2
; Sequence 2, Application US/09040005
; Patent No. 6057128
; GENERAL INFORMATION:
; APPLICANT: Donaldson, Debra
; TITLE OF INVENTION: MU-1 RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/040,005
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15320
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-498-8224
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 538 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-040-005-2

Query Match 100.0%; Score 1195; DB 3; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.5e-122; Indels 0; Gaps 0;
Matches 218; Conservative 0; Mismatches 0;
QY 1 CPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDYBELKDEATSCSLHRSAAHATHY 60
DB 20 CPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDYBELKDEATSCSLHRSAAHATHY 79
QY 61 TCHMDVFHMADDIFSVNITDQSGNYSQECGSLLAESIKPAPPNVTVTFSGQINISWR 120

Db 80 TCHMDVHFHMADDFSVNITDQSGNYSQCGSFLLAESIKPAPPNVVTFSGQYNISWR 139
QY 121 SYVEDPAFYMLKGLQYELQYRNKRGDPWAVSPRKLISVDSSVSLLEFRKDSSEYELQ 180
Db 140 SYVEDPAFYMLKGLQYELQYRNKRGDPWAVSPRKLISVDSSVSLLEFRKDSSEYELQ 199
QY 181 VRAGPMPGSSYQGTWSEWSDPVIFQTSBELKEGWNPH 218
Db 200 VRAGPMPGSSYQGTWSEWSDPVIFQTSBELKEGWNPH 237

RESULT 2

US-09-522-217-115
; Sequence 115, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: No. 6307024ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillion, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522, 217
; CURRENT FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-522-217-115

Query Match 100.0%; Score 1195; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.5e-122;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYEELEKDEATCSLHRSANATHATY 60
Db 20 CPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYEELEKDEATCSLHRSANATHATY 79
QY 61 TCHMDVHFHMADDFSVNITDQSGNYSQCGSFLLAESIKPAPPNVVTFSGQYNISWR 120
Db 80 TCHMDVHFHMADDFSVNITDQSGNYSQCGSFLLAESIKPAPPNVVTFSGQYNISWR 139
QY 121 SYVEDPAFYMLKGLQYELQYRNKRGDPWAVSPRKLISVDSSVSLLEFRKDSSEYELQ 180
Db 140 SYVEDPAFYMLKGLQYELQYRNKRGDPWAVSPRKLISVDSSVSLLEFRKDSSEYELQ 199
QY 181 VRAGPMPGSSYQGTWSEWSDPVIFQTSBELKEGWNPH 218
Db 200 VRAGPMPGSSYQGTWSEWSDPVIFQTSBELKEGWNPH 237

RESULT 3

US-09-404-641-2
; Sequence 2, Application US/09404641
; Patent No. 6576744
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.

; APPLICANT: No. 6576744ak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHA11
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/09/404,641
; CURRENT FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-404-641-2

Query Match 100.0%; Score 1195; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.5e-122;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYEELEKDEATCSLHRSANATHATY 60
Db 20 CPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYEELEKDEATCSLHRSANATHATY 79
QY 61 TCHMDVHFHMADDFSVNITDQSGNYSQCGSFLLAESIKPAPPNVVTFSGQYNISWR 120
Db 80 TCHMDVHFHMADDFSVNITDQSGNYSQCGSFLLAESIKPAPPNVVTFSGQYNISWR 139
QY 121 SYVEDPAFYMLKGLQYELQYRNKRGDPWAVSPRKLISVDSSVSLLEFRKDSSEYELQ 180
Db 140 SYVEDPAFYMLKGLQYELQYRNKRGDPWAVSPRKLISVDSSVSLLEFRKDSSEYELQ 199
QY 181 VRAGPMPGSSYQGTWSEWSDPVIFQTSBELKEGWNPH 218
Db 200 VRAGPMPGSSYQGTWSEWSDPVIFQTSBELKEGWNPH 237

RESULT 4

US-09-923-246-115
; Sequence 115, Application US/09923246
; Patent No. 6605272
; GENERAL INFORMATION:
; APPLICANT: No. 6605272ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillion, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-246-115

Query Match 100.0%; Score 1195; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.5e-122;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDQYBELKDEATSCSLHSAHNATHATY 60
DB 20 CPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDQYBELKDEATSCSLHSAHNATHATY 79
QY 61 TCHMDVHFHMADDFSVNITDQSGNYSCGSGFLAESIKPAPPFNVTVTFSGQYNISWR 120
DB 80 TCHMDVHFHMADDFSVNITDQSGNYSCGSGFLAESIKPAPPFNVTVTFSGQYNISWR 139
QY 121 SDYEDPAFYMLKGKLOQYELQYRNKGDPAWSPRKLISVDSRSVSLPLFRKDSSEYELQ 180
DB 140 SDYEDPAFYMLKGKLOQYELQYRNKGDPAWSPRKLISVDSRSVSLPLFRKDSSEYELQ 199
QY 181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
DB 200 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237

RESULT 5

US-10-295-723-115

; Sequence 115, Application US/10295723

; Patent No. 6686178

; GENERAL INFORMATION:

; APPLICANT: No. 6686178ak, Julia E.

; APPLICANT: Presnell, Scott R.

; APPLICANT: Sprecher, Cindy A.

; APPLICANT: Foster, Donald C.

; APPLICANT: Holly, Richard D.

; APPLICANT: Gross, Jane A.

; APPLICANT: Johnston, Janet V.

; APPLICANT: Nelson, Andrew J.

; APPLICANT: Dillon, Stacey R.

; APPLICANT: Hammond, Angela K.

; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND

; FILE REFERENCE: 99-16

; CURRENT APPLICATION NUMBER: US/10/295,723

; CURRENT FILING DATE: 2002-11-15

; PRIOR APPLICATION NUMBER: 09/522,217

; PRIOR FILING DATE: 2000-03-09

; PRIOR APPLICATION NUMBER: US 60/123,547

; PRIOR FILING DATE: 1999-03-09

; PRIOR APPLICATION NUMBER: US 60/123,904

; PRIOR FILING DATE: 1999-03-11

; PRIOR APPLICATION NUMBER: US 60/142,013

; PRIOR FILING DATE: 1999-07-01

; NUMBER OF SEQ ID NOS: 115

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 115

; TYPE: PRT

; LENGTH: 538

; ORGANISM: Homo sapiens

; US-10-295-723-115

Query Match 100.0%; Score 1195; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.5e-122;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDQYBELKDEATSCSLHSAHNATHATY 60
DB 20 CPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDQYBELKDEATSCSLHSAHNATHATY 79
QY 61 TCHMDVHFHMADDFSVNITDQSGNYSCGSGFLAESIKPAPPFNVTVTFSGQYNISWR 120
DB 80 TCHMDVHFHMADDFSVNITDQSGNYSCGSGFLAESIKPAPPFNVTVTFSGQYNISWR 139
QY 121 SDYEDPAFYMLKGKLOQYELQYRNKGDPAWSPRKLISVDSRSVSLPLFRKDSSEYELQ 180
DB 140 SDYEDPAFYMLKGKLOQYELQYRNKGDPAWSPRKLISVDSRSVSLPLFRKDSSEYELQ 199

QY 181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
DB 200 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237

RESULT 6

US-09-522-217-97

; Sequence 97, Application US/09522217

; Patent No. 6307024

; GENERAL INFORMATION:

; APPLICANT: No. 6307024ak, Julia E.

; APPLICANT: Presnell, Scott R.

; APPLICANT: Sprecher, Cindy A.

; APPLICANT: Foster, Donald C.

; APPLICANT: Holly, Richard D.

; APPLICANT: Gross, Jane A.

; APPLICANT: Johnston, Janet V.

; APPLICANT: Nelson, Andrew J.

; APPLICANT: Dillon, Stacey R.

; APPLICANT: Hammond, Angela K.

; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND

; FILE REFERENCE: 99-16

; CURRENT APPLICATION NUMBER: US/09/522,217

; CURRENT FILING DATE: 2000-03-09

; EARLIER APPLICATION NUMBER: US 60/123,547

; EARLIER FILING DATE: 1999-03-09

; EARLIER APPLICATION NUMBER: US 60/123,904

; EARLIER FILING DATE: 1999-03-11

; EARLIER APPLICATION NUMBER: US 60/142,013

; EARLIER FILING DATE: 1999-07-01

; NUMBER OF SEQ ID NOS: 115

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 97

; LENGTH: 606

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: MBP-zalphan1 soluble receptor polypeptide sequence

US-09-522-217-97

Query Match 100.0%; Score 1195; DB 4; Length 606;
Best Local Similarity 100.0%; Pred. No. 1.8e-122;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDQYBELKDEATSCSLHSAHNATHATY 60
DB 389 CPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDQYBELKDEATSCSLHSAHNATHATY 448
QY 61 TCHMDVHFHMADDFSVNITDQSGNYSCGSGFLAESIKPAPPFNVTVTFSGQYNISWR 120
DB 449 TCHMDVHFHMADDFSVNITDQSGNYSCGSGFLAESIKPAPPFNVTVTFSGQYNISWR 508
QY 121 SDYEDPAFYMLKGKLOQYELQYRNKGDPAWSPRKLISVDSRSVSLPLFRKDSSEYELQ 180
DB 509 SDYEDPAFYMLKGKLOQYELQYRNKGDPAWSPRKLISVDSRSVSLPLFRKDSSEYELQ 568
QY 181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
DB 569 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 606

RESULT 7

US-09-404-641-51

; Sequence 51, Application US/09404641

; Patent No. 6576744

; GENERAL INFORMATION:

; APPLICANT: Presnell, Scott R.

; APPLICANT: Conklin, Darrell C.

; APPLICANT: No. 6576744ak, Julia E.

; APPLICANT: Hammond, Angela K.

; TITLE OF INVENTION: CYTOKINE RECEPTOR ZALPHA11

; FILE REFERENCE: 98-55

; CURRENT APPLICATION NUMBER: US/09/404,641

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; CURRENT FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-09-404-641-51

Query Match      100.0%; Score 1195; DB 4; Length 606;
Best Local Similarity 100.0%; Pred. No. 1.8e-122;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDQYELKDEATSCSLHRSAAHNAATHY 60
DB 389 CPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDQYELKDEATSCSLHRSAAHNAATHY 448
QY 61 TCHMDVFHFMAADDIFSVNITDQSGNYSCGSGFLAELSIKPAPPFNVTTFSGQYNISWR 120
DB 449 TCHMDVFHFMAADDIFSVNITDQSGNYSCGSGFLAELSIKPAPPFNVTTFSGQYNISWR 508
QY 121 SYEDPAFYMLKGKQLQYELQYRNRGDPWAVSPRRKLIISVDSRSVSLLEPFKDKSSYELQ 180
DB 509 SYEDPAFYMLKGKQLQYELQYRNRGDPWAVSPRRKLIISVDSRSVSLLEPFKDKSSYELQ 568
QY 181 VRAGPMGSSYQGTWSESDPVIPTQSEELKEGWNPH 218
DB 569 VRAGPMGSSYQGTWSESDPVIPTQSEELKEGWNPH 606

RESULT 8
US-09-923-246-97
; Sequence 97, Application US/09923246
; Patent No. 6605272
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Gross, Richard D.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 97
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MBP-zalphall1 soluble receptor polypeptide sequence
US-09-923-246-97

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Query Match      100.0%; Score 1195; DB 4; Length 606;
Best Local Similarity 100.0%; Pred. No. 1.8e-122;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDQYELKDEATSCSLHRSAAHNAATHY 60
DB 389 CPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDQYELKDEATSCSLHRSAAHNAATHY 448
QY 61 TCHMDVFHFMAADDIFSVNITDQSGNYSCGSGFLAELSIKPAPPFNVTTFSGQYNISWR 120
DB 449 TCHMDVFHFMAADDIFSVNITDQSGNYSCGSGFLAELSIKPAPPFNVTTFSGQYNISWR 508
QY 121 SYEDPAFYMLKGKQLQYELQYRNRGDPWAVSPRRKLIISVDSRSVSLLEPFKDKSSYELQ 180
DB 509 SYEDPAFYMLKGKQLQYELQYRNRGDPWAVSPRRKLIISVDSRSVSLLEPFKDKSSYELQ 568
QY 181 VRAGPMGSSYQGTWSESDPVIPTQSEELKEGWNPH 218
DB 569 VRAGPMGSSYQGTWSESDPVIPTQSEELKEGWNPH 606

RESULT 9
US-10-295-723-97
; Sequence 97, Application US/10295723
; Patent No. 6686178
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Gross, Richard D.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 97
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MBP-zalphall1 soluble receptor polypeptide sequence
US-10-295-723-97

Query Match      100.0%; Score 1195; DB 4; Length 606;
Best Local Similarity 100.0%; Pred. No. 1.8e-122;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDQYELKDEATSCSLHRSAAHNAATHY 60
DB 389 CPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDQYELKDEATSCSLHRSAAHNAATHY 448
QY 61 TCHMDVFHFMAADDIFSVNITDQSGNYSCGSGFLAELSIKPAPPFNVTTFSGQYNISWR 120
DB 449 TCHMDVFHFMAADDIFSVNITDQSGNYSCGSGFLAELSIKPAPPFNVTTFSGQYNISWR 508
QY 121 SYEDPAFYMLKGKQLQYELQYRNRGDPWAVSPRRKLIISVDSRSVSLLEPFKDKSSYELQ 180
DB 509 SYEDPAFYMLKGKQLQYELQYRNRGDPWAVSPRRKLIISVDSRSVSLLEPFKDKSSYELQ 568

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QY 181 VRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
Best Local Similarity 69.3%; Pred. No. 5.2e-84;
Matches 151; Conservative 31; Mismatches 36; Indels 0; Gaps 0;

Db 569 VRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 606
RESULT 10
US-09-404-641-85
; Sequence 85, Application US/09404641
; Patent No. 6576744
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. 6576744ak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHAIL
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/09/404,641
; CURRENT FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Mus musculus

US-09-404-641-85
Query Match 70.6%; Score 844; DB 4; Length 529;
Best Local Similarity 69.3%; Pred. No. 5.2e-84;
Matches 151; Conservative 31; Mismatches 36; Indels 0; Gaps 0;

2y 1 CPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQOYBELKDEATSCSLHRSANATHATY 60
Db 20 CLDLTCYTDYLTQVICILEMNNLHPSTLTLTWQOYBELKDEATSCSLHRSANATHATY 79
2y 61 TCHMDVHFHMAADDIPSVNITDQSGNYSCGCSFLLAESIKPAPPFNVTTFSGQYNISMR 120
Db 80 TCHMRLSQFLSDSEFVIVNVTQSGNNSQECGSFVLAESIKPAPPFNVTTFSGQYNISMR 139
2y 121 SYEDPAPFVLMKGLQYELQYRNLRDPAVSPRKLISVDSRSVSLPLFRKDSYELQ 180
Db 140 SAYDEPSNYVLRGKGLQYELQYRNLRDPAVSPRKLISVDSRSVSLPLFRKDSYELQ 199
2y 181 VRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
Db 200 VRAAPQPGTSFRGTWSEWSDPVIFQTQAGEPEAGWDPH 237

RESULT 11
US-09-732-234-6
; Sequence 6, Application US/09732234
; Patent No. 6586251
; GENERAL INFORMATION:
; APPLICANT: Murphy, et al.
; TITLE OF INVENTION: METHODS OF MODIFYING EUKARYOTIC CELLS
; FILE REFERENCE: REG 780A
; CURRENT APPLICATION NUMBER: US/09/732,234
; CURRENT FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mouse Ocr10 protein
US-09-732-234-6

Query Match 70.1%; Score 838; DB 4; Length 529;
Best Local Similarity 68.3%; Pred. No. 2.4e-83;
Matches 149; Conservative 33; Mismatches 36; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQOYBELKDEATSCSLHRSANATHATY 60
Db 20 CLDLTCYTDYLTQVICILEMNNLHPSTLTLTWQOYBELKDEATSCSLHRSANATHATY 79
QY 61 TCHMDVHFHMAADDIPSVNITDQSGNYSCGCSFLLAESIKPAPPFNVTTFSGQYNISMR 120
Db 80 TCHMRLSQFLSDSEFVIVNVTQSGNNSQECGSFVLAESIKPAPPFNVTTFSGQYNISMR 139
QY 121 SYEDPAPFVLMKGLQYELQYRNLRDPAVSPRKLISVDSRSVSLPLFRKDSYELQ 180
Db 140 SAYDEPSNYVLRGKGLQYELQYRNLRDPAVSPRKLISVDSRSVSLPLFRKDSYELQ 199
QY 181 VRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
Db 200 MEAAPQPGTSFRGTWSEWSDPVIFQTQAGEPEAGWDPH 237
RESULT 12
US-09-784-859-6
; Sequence 6, Application US/09784859
; Patent No. 6596541
; GENERAL INFORMATION:
; APPLICANT: Murphy, et al.
; TITLE OF INVENTION: METHODS OF MODIFYING EUKARYOTIC CELLS
; FILE REFERENCE: REG 780B
; CURRENT APPLICATION NUMBER: US/09/784,859
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mouse Ocr10 protein
US-09-784-859-6

Query Match 70.1%; Score 838; DB 4; Length 529;
Best Local Similarity 68.3%; Pred. No. 2.4e-83;
Matches 149; Conservative 33; Mismatches 36; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQOYBELKDEATSCSLHRSANATHATY 60
Db 20 CLDLTCYTDYLTQVICILEMNNLHPSTLTLTWQOYBELKDEATSCSLHRSANATHATY 79
QY 61 TCHMDVHFHMAADDIPSVNITDQSGNYSCGCSFLLAESIKPAPPFNVTTFSGQYNISMR 120
Db 80 TCHMRLSQFLSDSEFVIVNVTQSGNNSQECGSFVLAESIKPAPPFNVTTFSGQYNISMR 139
QY 121 SYEDPAPFVLMKGLQYELQYRNLRDPAVSPRKLISVDSRSVSLPLFRKDSYELQ 180
Db 140 SAYDEPSNYVLRGKGLQYELQYRNLRDPAVSPRKLISVDSRSVSLPLFRKDSYELQ 199
QY 181 VRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
Db 200 MEAAPQPGTSFRGTWSEWSDPVIFQTQAGEPEAGWDPH 237
RESULT 13
US-09-404-641-81
; Sequence 81, Application US/09404641
; Patent No. 6576744
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. 6576744ak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHAIL

```
FILE REFERENCE: 98-55
CURRENT APPLICATION NUMBER: US/09/404,641
CURRENT FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/100,896
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: US 60/123,546
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/142,574
PRIOR FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 91
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 81
LENGTH: 397
TYPE: PRT
ORGANISM: Mus musculus
US-09-404-641-81

Query Match 33.5%; Score 400; DB 4; Length 397;
Best Local Similarity 68.6%; Pred. No. 1.9e-35;
Matches 72; Conservative 18; Mismatches 15; Indels 0; Gaps 0;

QY 114 QYNISWRSDYEDPAFYMLKGLQYELQYVNRGDPWAVSPRKLISVDSRSVSLPLBFRK 173
DB 1 RYDISWSDAYDEFSNYLRLKGLQYELQYVNRGDPWAVSPRKLISVDSRSVSLPLBFRK 60

QY 174 DSSYELQVNRGDPWPGSSYOGTWSEWSDPVIPTQSEELKEGWNPH 218
DB 61 DSSYELQVNRGDPWPGSSYOGTWSEWSDPVIPTQSEELKEGWNPH 105

RESULT 14
US-08-780-562-7
Sequence 7, Application US/08/780562
Patent No. 6541604
GENERAL INFORMATION:
APPLICANT: Matthews, William
APPLICANT: Bennett, Brian
TITLE OF INVENTION: WSX RECEPTOR
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,562
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585005
FILING DATE: 01/08/97
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/
FILING DATE: 01/08/97
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0986R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 amino acids
TYPE: Amino Acid
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TOPOLOGY: Linear
US-08-780-562-7

Query Match 12.1%; Score 144; DB 4; Length 783;
Best Local Similarity 31.1%; Pred. No. 6.5e-07;
Matches 57; Conservative 22; Mismatches 60; Indels 44; Gaps 11;

QY 39 LKDE---ATSCSLHRSNAHATHATYTHMDVFH-----FMADDIFSVNITDQSGNYS 87
DB 177 LKDSFQTVQCNSLRGC-----ECHVPVPRAKLNYALIMYLEITTSAGVSFOSPLMS 227

QY 88 QEGSGFLLAESIKPAPP--FNVTVTFSGQYNISWSDYEDPAFYMLKGLQYELQYVNRG 145
DB 228 LQ--PMLV---VKDPPLGLHMEVTDGMLKISWDSQTWAPP-----PLQYQVXLENS 276

QY 146 DPWAVSPRKLISVDSRSV-SLLPLEFRKDSSEYELQVNRGPMGSSYOGTWSEWSDPVI 204
DB 277 T--IVREAAEIVSATSLLDVSLP-----GSSYEYQVRSKRDLGS---GVNSDWSSPQVF 326

QY 205 QTQ 207
DB 327 TTQ 329

RESULT 15
US-08-599-455B-2
Sequence 2, Application US/08/599455B
Patent No. 5972621
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
MODULATE BODY WEIGHT USING THE OB RECEPTOR
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,455B
FILING DATE: 22-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/017001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 894 amino acids
TYPE: amino acid
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TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-599-455B-2

Query Match 12.1%; Score 144; DB 2; Length 894;
Best Local Similarity 31.1%; Pred. No. 7.9e-07;
Matches 57; Conservative 22; Mismatches 60; Indels 44; Gaps 11;
2y 39 LKDE----ATSCSLHRSAHNATHATYTCMDVPH-----FWADDIFSVNITDQSGNYS 87
Db 177 LKSFQTVQCNCSLRGC-----ECHVPVPRAKLNLYALLMYLEITSAGVSFQSPPLMS 227
2y 88 QECGSFLLAESIKPAPF--FNVTVTFSGQYNISWRSDYEDPAFWMLKGLQYELQYRNRG 145
Db 228 LQ--PMLV---VKDPDPLGLHMEVTDGDLKISWDSQTMAPF-----PQYQVKYLENS 276
2y 146 DPWAVSPRRKLIISVDSRSV-SLLPLEPRKDSYELQVRAGMPGSSYQGTWSEWSDPVIF 204
Db 277 T--IVREAAEIVSATSLLDVSVLP-----GSSYEYQVRSKRLDGS---GWSWSSPQVF 326
2y 205 QTQ 207
Db 327 TTQ 329

Search completed: March 3, 2004, 12:39:55
Job time : 15.317 secs

GenCore version 5.1.6
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3M protein - protein search, using sw model

Run on: March 3, 2004, 12:25:04 ; Search time 8.19281 Seconds
(without alignments)

1385.519 Million cell updates/sec

Title: US-09-825-561A-6

Perfect score: 1195

Sequence: 1 CPDLVCYDYLTQVVICILEM.....SDPVIFQTQSEELKEGWNPH 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	1195	100.0	538	1 I21R HUMAN	Q9hbe5 homo sapien
2	844	70.6	529	1 I21R MOUSE	Q9jhx3 mus musculus
3	145	12.1	878	1 IL3B MOUSE	P26954 mus musculus
4	144	12.1	896	1 CYRB MOUSE	P26955 mus musculus
5	144	12.1	1162	1 LEPR MOUSE	P48356 mus musculus
6	141.5	11.8	539	1 IL2B MOUSE	P16297 mus musculus
7	139	11.6	635	1 TPOR HUMAN	P40238 homo sapien
8	138	11.5	1162	1 LEPR RAT	Q62959 rattus norv
9	137	11.5	1165	1 LEPR HUMAN	P48357 homo sapien
10	135.5	11.3	825	1 IL4R HUMAN	P24394 homo sapien
11	135	11.3	1163	1 LEPR MACMU	Q9mvl0 macaca mula
12	134	11.2	537	1 IL2B RAT	P26896 rattus norv
13	133.5	11.2	369	1 CYRG MOUSE	P34902 mus musculus
14	132.5	11.1	625	1 TPOR MOUSE	Q08351 mus musculus
15	129	10.8	1165	1 LEPR PIG	O02671 sus scrofa
16	127.5	10.7	379	1 CYRG BOVIN	Q95118 bos taurus
17	127	10.6	373	1 CYRG CANFA	P40321 canis famil
18	126	10.5	551	1 IL2B HUMAN	P14784 homo sapien
19	123	10.3	459	1 IL7R HUMAN	P16871 homo sapien
20	122	10.2	831	1 PRLR CHICK	Q04594 gallus gall
21	121.5	10.2	918	1 IL6B RAT	P40190 rattus norv
22	120	10.0	369	1 CYRG HUMAN	P31785 homo sapien
23	118.5	9.9	862	1 IL2S HUMAN	Q99665 homo sapien
24	118	9.9	897	1 CYRB HUMAN	P32927 homo sapien
25	117	9.8	810	1 IL4R MOUSE	P16382 mus musculus
26	115.5	9.7	831	1 PRLR MELGA	Q91094 meleagris g
27	115	9.6	459	1 IL7R MOUSE	P16872 mus musculus
28	112.5	9.4	917	1 IL6B HUMAN	Q00560 mus musculus
29	110.5	9.2	918	1 IL6B MOUSE	P40189 homo sapien
30	108.5	9.1	638	1 IL6A HUMAN	P08887 homo sapien
31	106	8.9	468	1 GHR PIG	P19756 sus scrofa
32	105.5	8.8	460	1 IL6A MOUSE	P22272 mus musculus
33	105.5	8.8	638	1 GHR RAT	P16310 rattus norv

ALIGNMENTS

```

RESULT 1
121R HUMAN
ID I21R HUMAN STANDARD; PRT; 538 AA.
AC Q9HBE5; Q96HZ1; Q9HB91;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Interleukin 21 receptor precursor (IL-21R) (Novel interleukin
DE receptor).
GN IL21R OR NLR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

SEQUENCE FROM N.A.
RX MEDLINE=20531754; PubMed=11081504;
RA Parrish-Novak J., Dillon S.R., Nelson A., Hammond A., Sprecher C.,
RA Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader S.,
RA Burkhead S., Heipel M., Brandt C., Kuilper J.L., Kramer J.,
RA Conklin D., Fressnell S.R., Berry J.J., Shioa F., Bort S., Hamby K.,
RA Mudri S., Clegg C., Moore M., Grant F.J., Lofton-Day C., Gilbert T.,
RA Raymond F., Ching A., Yao L., Smith D., Webster P., Whitmore T.,
RA Maurer M., Kaushansky K., Holly R.D., Foster D.;
RA "Interleukin 21 and its receptor are involved in NK cell expansion and
RA regulation of lymphocyte function.";
RL Nature 408:57-63(2000).

SEQUENCE FROM N.A.
RX MEDLINE=20481926; PubMed=11016959;
RA Ozaki K., Kikly K., Michalovich D., Young P.R., Leonard W.J.;
RA "Cloning of a type I cytokine receptor most related to the IL-2
RA receptor beta chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:11439-11444(2000).

SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie H.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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34 105 8.8 522 1 IL9R HUMAN Q01113 homo sapien
35 104 8.7 638 1 GHR RABIT P19941 oryctolagus
36 103 8.6 508 1 EPOR HUMAN P19235 homo sapien
37 102 8.5 468 1 IL9R MOUSE Q01114 mus musculus
38 99.5 8.3 467 1 IL6A PIG O18796 sus scrofa
39 99.5 8.3 507 1 EPOR MOUSE P14753 mus musculus
40 99 8.3 420 1 IL5R HUMAN Q01344 homo sapien
41 97.5 8.2 662 1 IL2R HUMAN P42701 homo sapien
42 97 8.1 462 1 IL6A RAT P22273 rattus norv
43 95 7.9 415 1 IL5R MOUSE P21183 mus musculus
44 95 7.9 581 1 PRLR CEREL Q28235 cervus elap
45 94 7.9 328 1 IL2B MACMU P48095 macaca mula

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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Griewood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzwinski M.L., Skalska U., Smalus D.B., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RL -!- FUNCTION: This is a receptor for interleukin-21.

CC -!- SUBUNIT: Heterodimer with the common gamma chain. Associates with JAK1.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: Selectively expressed in lymphoid tissues. Most highly expressed in thymus and spleen.

CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors. Subfamily 4.

CC -!- SIMILARITY: Contains 1 fibronectin type III domain.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/) or send an email to license@isb-sib.ch).

CC EMBL; AF254067; AAG29346.1; -

DR EMBL; AF269133; AAG23419.1; -

DR EMBL; AY064474; AAL39168.1; -

DR EMBL; BC004348; AAH04348.1; -

DR EMBL; BC007946; AAH07946.1; -

DR Genbank; HGNC:6006; IL21R.

DR MIM; 605383; -

DR GO; GO:0046021; C: integral to membrane; NAS.

DR GO; GO:0001532; F: interleukin-21 receptor activity; NAS.

DR GO; GO:0030101; P: natural killer cell activation; NAS.

DR InterPro; IPR003961; FN III.

DR InterPro; IPR003531; Hemoptoptn_S_F1.

DR SMART; SM00060; FN3; 1.

DR PROSITE; PS01355; HEMATOPO_REC_S_F1; FALSE_NEG.

KW Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism.

FT SIGNAL 1 19 POTENTIAL.

FT CHAIN 20 538 INTERLEUKIN 21 RECEPTOR.

FT DOMAIN 20 232 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 233 253 POTENTIAL.

FT DOMAIN 254 538 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 120 209 FIBRONECTIN TYPE-III.

FT DISULFID 25 35 BY SIMILARITY.

FT POTENTIAL 65 81 POTENTIAL.

FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARIANT 131 191 R -> C (in dbSNP:3093370).

FT FTIC=VAR 014360.

FT S -> R (in dbSNP:3093385).

FT FTIC=VAR 014361.

FT G -> S (in dbSNP:3093386).

FT FTIC=VAR 014362.

FT AVP -> HEA (IN REF. 4; AAH07946).

FT G -> R (IN REF. 2).

FT SEQUENCE 538 AA; 59129 MW; 414079CCB974850A CRC64;

Query Match 100.0%; Score 1195; DB 1; Length 538;

Best Local Similarity 100.0%; Pred. No. 1.1e-96;

Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYDYLQTVICILEMNLHSTLTWQDYELKDEATSCSLRRAHNAATHATY 60

DB 20 CPDLVCYDYLQTVICILEMNLHSTLTWQDYELKDEATSCSLRRAHNAATHATY 79

QY 61 TCHMDVHFHMADIFSVNITDQSGNYSCGSLFLAESIKPAPPFNVTFTSGQYNISWR 120

Db 80 TCHMDVHFHMADIFSVNITDQSGNYSCGSLFLAESIKPAPPFNVTFTSGQYNISWR 139

QY 121 SYEDPAPFMYLKGKLOYELQVNRGDPWAVSPRKLISVDSESYLLPLEKDSYELQ 180

Db 140 SYEDPAPFMYLKGKLOYELQVNRGDPWAVSPRKLISVDSESYLLPLEKDSYELQ 199

QY 181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218

Db 200 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237

RESULT 2

ID 121R MOUSE STANDARD; PRT; 529 AA.

AC Q9JHX3; Q9BSML; 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Interleukin 21 receptor precursor (IL-21R) (Novel interleukin DE receptor) (lymphocyte receptor beta) (LR-beta) (Novel cytokine DE receptor NR8).

GN IL21R OR NLR.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; OC Mammalia; Eutharia; Rodentia; Sciurognathi; Muridae; Mus.

OC NCBI_taxid=10090;

OX [1]

RN SEQUENCE FROM N.A.

RP STRAIN=C57BL/6;

RC MEDLINE=20531754; PubMed=11081504;

RX Parrish-Novak J., Dillon S.R., Nelson A., Hammond A., Sprecher C., Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader S., Burkhead S., Heipel M., Brandt C., Kuipjer J.L., Kramer J., Conklin D., Presnell S.R., Berry J., Shota F., Bort S., Hamby K., Mudri S., Clegg C., Moore M., Grant F.J., Lofton-Day C., Gilbert T., Raymond F., Ching A., Yao L., Smith D., Webster P., Whitmore T., Maurer M., Kaushansky K., Holly R.D., Foster D.; "Interleukin 21 and its receptor are involved in NK cell expansion and regulation of lymphocyte function.";

RT Nature 408:57-63(2000).

RL [2]

RN SEQUENCE FROM N.A.

RP TISSUE=Spleen, and Thymus;

RC MEDLINE=20481926; PubMed=11016959;

RX Ozaki K., Kikly K., Michalovich D., Young P.R., Leonard W.J.; "Cloning of a type I cytokine receptor most related to the IL-2 receptor beta chain.";

RT Proc. Natl. Acad. Sci. U.S.A. 97:11439-11444(2000).

RL [3]

RN SEQUENCE FROM N.A.

RP Donaldson D.D., Whitters M.J., Fitz L., Unger M., Finnerty H., Dagdigian C., Lowe L., Wood C.R., Young D.A., Collins M.; "Chromosome 16p12 encodes a biologically active IL-2Rb related receptor with lymphoid restricted expression.";

RT Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

RL [4]

RN SEQUENCE FROM N.A.

RP STRAIN=BALB/c;

RC Nomura H., Yaguchi N., Maeda M., Hasegawa M.; "A novel cytokine receptor NR8 is closely mapped to IL-4R: polymorphism in Balb/c mouse.";

RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

RL [5]

RN SEQUENCE FROM N.A.

RP STRAIN=A/J, B10.S/DvTe, C57BL/6J, NOD/LtJ, and SJL/J; TISSUE=Spleen;

RC Gao J., Teuscher C.; "Mus musculus interleukin 21 receptor Gene Il21r mRNA.";

RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

RL -!- FUNCTION: This is a receptor for interleukin-21

CC -!- SUBUNIT: Heterodimer with the common gamma chain. Associates with JAK1.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: Selectively expressed in lymphoid tissues.

CC Most highly expressed in thymus and spleen.
 CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
 CC Subfamily 4.
 CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AF254068; AAG29347.1; -
 CC EMBL; AF269134; AAG24240.1; -
 CC EMBL; AF293436; AAF86350.1; -
 CC EMBL; AB049137; BAB13736.1; -
 CC EMBL; AF477982; AAL82632.1; -
 CC EMBL; AF477983; AAL82633.1; -
 CC EMBL; AF477984; AAL82634.1; -
 CC EMBL; AF477985; AAL82635.1; -
 CC EMBL; AF477986; AAL82636.1; -
 CC MGD; MGI:1890475; I21r.
 CC GO; GO:0004907; F:interleukin receptor activity; IDA.
 CC InterPro; IPR008957; FN.III-like.
 CC InterPro; IPR003961; FN.III.
 CC InterPro; IPR007110; Ig-like.
 CC SMART; SM00060; FN3; 1.
 CC PROSITE; PS01355; HEMATOPO_REC_S_F1; FALSE NEG.
 CC Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism.
 CC SIGNAL 1 19
 CC CHAIN 20 529
 CC DOMAIN 20 238
 CC TRANSMEM 238 258
 CC DOMAIN 259 529
 CC DOMAIN 120 209
 CC DISULFID 25 35
 CC CARBOHYD 65 81
 CC CARBOHYD 73 73
 CC CARBOHYD 97 97
 CC CARBOHYD 104 104
 CC CARBOHYD 125 125
 CC CARBOHYD 182 182
 CC VARIANT 69 69
 CC VARIANT 200 200
 CC SEQUENCE 529 AA; 58354 MW; 8B41816B0D426581 CRC64;
 SQ
 Query Match 70.6%; Score 844; DB 1; Length 529;
 Best Local Similarity 69.3%; Pred. No. 4.1e-66;
 Matches 151; Conservative 31; Mismatches 36; Indels 0; Gaps 0;
 QY 1 CPDLVCYDYLTQVTCILEMNLHPSTLTLTWQDYBELKDEATSCSLHRSAAHATHATY 60
 Db 20 CLDLTCYDYLTQVTCILEMNLHPSTLTLTWQDYBELKDEATSCSLHRSAAHATHATY 79
 QY 61 TCHMDVHFMAADDIPSNITQSGNYSCEGSPFLAESIKPAPFNVTVPFGQYNISWR 120
 Db 80 TCHMPLSQFLSDVEFVNTQSGNNSCEGSPFLAESIKPAPFNVTVPFGQYDISWD 139
 QY 121 SDYEDPAFYMLKGLQYELQVNRDGPVAVPRKLLISVDSRSVLLPLPRKDSSEYELQ 180
 Db 140 SAYDEPSNVYLGKQLQYELQVNRDGPVAVPRKLLISVDSRSVLLPLPRKDSSEYELQ 199
 QY 181 VRAGMPGSSVGGTWSWSDPVIPTQSEELKEGNPH 218
 Db 200 VRAAPQPGTSPRGTWSEWSDPVIPTQAGEPEAGWDPH 237
 RESULT 3
 IL3B_MOUSE
 ID IL3B_MOUSE PRT; 878 AA.
 AC P26954;

DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Interleukin-3 receptor class II beta chain precursor (Colony
 DE stimulating factor 2 receptor, beta 2 chain).
 GN CSF2RB2 OR A12CA OR IL3RB2 OR IL3R.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90117145; PubMed=2404337;
 RA Itoh N., Yonehara S., Schreurs J., Gorman D.M., Maruyama K., Ishii A.,
 RA Yanara I., Arai K., Miyajima A.;
 RT "Cloning of an interleukin-3 receptor gene: a member of a distinct
 RT receptor gene family.";
 RL Science 247:324-327(1990).
 CC -!- FUNCTION: In mouse, there are two classes of high-affinity IL3
 CC receptors. One contains this IL3-specific beta chain and the other
 CC contains the beta chain also shared by high-affinity IL5 and GM-
 CC CSF receptors.
 CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
 CC Subfamily 4.
 CC
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 CC
 CC EMBL; M29855; AAA39295.1; -
 CC PIR; A40091; A40091.
 CC MGD; MGI:1339760; Csf2rb2.
 CC InterPro; IPR002996; CRIA.
 CC InterPro; IPR00282; Cytok_receptor_2.
 CC InterPro; IPR008957; FN.III-like.
 CC InterPro; IPR003961; FN.III.
 CC InterPro; IPR003531; Hemtopoptn_S_F1.
 CC Pfam; PF00041; fn3; 2.
 CC SMART; SM00060; FN3; 2.
 CC PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
 CC Receptor; Transmembrane; Glycoprotein; Signal.
 CC SIGNAL 1 22
 CC CHAIN 23 878
 CC DOMAIN 23 440
 CC TRANSMEM 441 462
 CC DOMAIN 463 878
 CC DISULFID 39 49
 CC DISULFID 78 95
 CC DISULFID 254 264
 CC DISULFID 293 310
 CC CARBOHYD 350 350
 CC SEQUENCE 878 AA; 97195 MW; 8EBC9092ADC24D56 CRC64;
 SQ
 Query Match 12.1%; Score 145; DB 1; Length 878;
 Best Local Similarity 23.0%; Pred. No. 6.2e-05;
 Matches 48; Conservative 38; Mismatches 97; Indels 26; Gaps 7;
 QY 3 DLVCTDYLTQVTCILEMNLHPSTLTLTWQDYBELKDEATSCSLHRSAAHATHATY 62
 Db 251 NLQCFDGIQSLHCSWEVWVTTQTSVGLFYRPPAPAEKSPVKEPQASVVVTRVC 310
 QY 63 HMDVHFMAADDIPSNITQSGNYSCEGSPFLAESIKPAPFNVTVPFGQYNISWR 121
 Db 311 SLVPEPSAHSQITVSX-----HLEQKFTMSYTHIQMEPPIINQTKNRDYSLSHWET 364

QY 122 D-----YEDPAFYMLKGLQYELVNRGDPWAVSPRKLISVDSRSVSLPLPFRKDSY 177
 DB 365 QXIPKIDHTF-----QVYKKSSEKSDKSTENLGRVNSMD---LP-QLEPDTSY 411

QY 178 ELQVRAGMPGSSYQGTWSESDPVIFOT 206
 DB 412 CARVRVKPI--SDYGIWSEWSNEVWTWT 438

RESULT 4
 CYRB MOUSE
 ID CYRB MOUSE STANDARD; PRT; 896 AA.
 AC P26955;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cytokine receptor common beta chain precursor (CDw131 antigen) (GM-
 CSF/IL-3/IL-5 receptor common beta-chain).
 GN CSF2RB OR CSF2RB1 OR AIC2B OR IL3RB1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90319131; PubMed=1695379;
 RA Gorman D.M., Itoh N., Kitamura T., Schreurs J., Yorehara S.,
 RA Yahara I., Arai K., Miyajima A.;
 RT "Cloning and expression of a gene encoding an interleukin 3 receptor-
 like protein: identification of another member of the cytokine
 receptor gene family";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:5459-5463(1990).
 CC -!- FUNCTION: High affinity receptor for interleukin-3, interleukin-5
 and granulocyte-macrophage colony-stimulating factor.
 CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain. The beta chain
 is common to the IL3, IL5 and GM-CSF receptors.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
 CC Subfamily 4.
 CC -!- SIMILARITY: Contains 2 fibronectin type III domains.

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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M34397; AAA37204.1; --
 DR FIR; A35782; A35782.
 DR MGD; MG1:1339759; Csf2rb1.
 DR InterPro; IPR002996; CRIA.
 DR InterPro; IPR000282; Cytok_receptor_2.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR003961; FN_III.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00060; FN3; 2.
 DR PROSITE; PS01355; HEWATOPO_REC_S_F1; 1.
 KW Receptor; transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 896 CYTOKINE RECEPTOR COMMON BETA CHAIN.
 FT DOMAIN 23 441 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 442 463 POTENTIAL.
 FT DOMAIN 464 896 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 132 241 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 343 440 FIBRONECTIN TYPE-III 2.
 FT DISULFID 39 49 BY SIMILARITY.
 FT DISULFID 77 99 BY SIMILARITY.
 FT DISULFID 88 94 BY SIMILARITY.
 FT DISULFID 253 263 BY SIMILARITY.
 FT DISULFID 292 310 BY SIMILARITY.
 FT CARBOHYD 62 62 N-LINKED (GLCNAC...) (POTENTIAL).

FT CARBOHYD 141 141 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 350 350 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 896 AA; 99111 MW; 8C516DFDC07A999 CRC64;

Query Match 12.1%; Score 144; DB 1; Length 896;
 Best Local Similarity 22.6%; Pred. No. 7.7e-05;
 Matches 49; Conservative 41; Mismatches 87; Indels 40; Gaps 9;

QY 3 DLVCTDYLTQVTCILEMWN-----LHPSTLTITWQDYEEELKDEATSCSLHRS 51
 DB 250 NLQCFDGIQSLHCSWEVWVTTGTSVSGLFTRPSFVA-----PEKCSVPVKEP 299
 QY 52 AHNATHATYTCHEMDVHFHFNADIFSVNITDQSGNYSQECGSFLLA-ESIKPAPP-FNVTV 109
 DB 300 PGASVVTYRCHSLPVPPESAHQYTVSVK-----HLEQGFIMSYNHIQMEPTLNLTK 353
 QY 110 TFSQYNIWRSRDYEDPAFYMLKGLQYELVNRGDPWAVSPRKLISVDSRSVSLPL 169
 DB 354 N-RDSYSLHWETQKWAYSFI-----EHTFOVYKKSKSDSWEDSKTENLDRHNSMDLS--- 404
 QY 170 EFRKDSYELQVRAGMPGSSYQGTWSESDPVIFOT 206
 DB 405 QLEPDTSYCARVRVKPI--SNYDGIWSEWSNEVWTWT 439

RESULT 5
 LEPR MOUSE
 ID LEPR MOUSE STANDARD; PRT; 1162 AA.
 AC P48356; O35686; O54986; Q61215; Q64309; Q9QWV5;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Leptin receptor precursor (LEP-R) (OB receptor) (OB-R) (B219).
 GN LEP-R OR OBR OR DB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RC TISSUE=Choroid plexus;
 RX MEDLINE=96128129; PubMed=8548812;
 RA Tartaglia L.A., Dembski M., Weng X., Deng N., Culpepper J.,
 RA Davos R., Richards G.J., Campfield L.A., Clark P.T., Deeds J.,
 RA Muir C., Sanker S., Moriarty A., Moore K.J., Smutko J.S.,
 RA Mays G.G., Wolf E.A., Monroe C.A., Tepper R.I.;
 RT "Identification and expression cloning of a leptin receptor, OB-R";
 RL Cell 83:1263-1271(1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM B).
 RC STRAIN=C57BL/KsJ; TISSUE=Hypothalamus;
 RX MEDLINE=96130816; PubMed=8608603;
 RA Chen H., Charlat O., Tartaglia L.A., Wolf E.A., Weng X.,
 RA Ellis S.J., Lakey N.D., Culpepper J., Moore K.J., Breitbart R.E.,
 RA Duyk G.M., Tepper R.I., Morgenstern J.P.;
 RT "Evidence that the diabetes gene encodes the leptin receptor:
 RT identification of a mutation in the leptin receptor gene in db/db
 mice";
 RL Cell 84:491-495(1996).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS A; B; C; D AND E).
 RC STRAIN=C57BL/Ks; TISSUE=Hypothalamus;
 RX MEDLINE=96231937; PubMed=8628397;
 RA Lee G.-H., Proenca R., Montez J.M., Carroll K.M., Darvishzadeh J.G.,
 RA Lee J.I., Friedman J.M.;
 RT "Abnormal splicing of the leptin receptor in diabetic mice";
 RL Nature 379:632-635(1996).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM C).
 RC STRAIN=BALB/c; TISSUE=Liver;
 RX MEDLINE=96206286; PubMed=8616721;
 RA Cioffi J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J.,
 RA Mikhail A., Platika D., Snodgrass H.R.;

"Novel B219/OB receptor isoforms: possible role of leptin in hematoopoiesis and reproduction."; Nat. Med. 2:585-589(1996). [5]

SEQUENCE FROM N.A. (ISOFORM B). STRAIN=NZO; TISSUE=Hypothalamus; MEDLINE=97462708; PubMed=9322935; Igel M., Becker W., Herberg L., Joest H.G.; "Hyperleptinemia, leptin resistance, and polymorphic leptin receptor in the New Zealand obese mouse."; Endocrinology 138:4234-4239(1997). [6]

SEQUENCE FROM N.A. (ISOFORMS A AND B). STRAIN=FVB/N; TISSUE=Spleen; MEDLINE=96270520; PubMed=8692797; Ghilardi N., Ziegler S., Wiestner A., Stoffel R., Heim M.H., Skoda R.C.; "Defective STAT signaling by the leptin receptor in diabetic mice."; Proc. Natl. Acad. Sci. U.S.A. 93:6231-6235(1996). [7]

SEQUENCE FROM N.A. (ISOFORMS A; B; C AND E). STRAIN=129/J; MEDLINE=98008913; PubMed=9344648; Chua S.C., Koutiras I.K., Han L., Liu S.M., Kay J., Young S.J., Chung W.K., Leibell R.L.; "Fine structure of the murine leptin receptor gene: splice site suppression is required to form two alternatively spliced transcripts."; Genomics 45:264-270(1997). [8]

SEQUENCE FROM N.A. (ISOFORM B), AND VARIANT ASN-600. STRAIN=KK Obese; TISSUE=Hypothalamus; MEDLINE=99061814; PubMed=9845674; Igel M., Taylor B.A., Phillips S.J., Becker W., Herberg L., Joest H.G.; "Hyperleptinemia and leptin receptor variant Asp600Asn in the obese, hyperinsulinemic KK mouse strain."; J. Endocrinol. 21:337-345(1998). [9]

SEQUENCE OF 890-1162 FROM N.A. (ISOFORM B). STRAIN=129; Banks A.S., Myers M.G. Jr.; "Murine leptin receptor genomic exon 18b and surrounding sequence."; Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases. [10]

PHOSPHORYLATION OF TYR-985 AND TYR-1138, AND MUTAGENESIS OF TYR-985; TYR-1077 AND TYR-1138. MEDLINE=20261588; PubMed=10799542; Banks A.S., Davis S.M., Bates S.H., Myers M.G. Jr.; "Activation of downstream signals by the long form of the leptin receptor."; J. Biol. Chem. 275:14563-14572(2000).

-!- FUNCTION: Receptor for obesity factor (leptin). Involved in the regulation of fat metabolism and in a hematopoietic pathway required for normal lymphopoiesis. May play a role in reproduction.

-!- FUNCTION: The short form (isoform A) may act to transport leptin to the cerebrospinal fluid. The putative soluble receptor (isoform E) could function as a transport protein.

-!- SUBCELLULAR LOCATION: Type I membrane protein. Except for form E which could be secreted.

-!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=5; Name=B; IsoId=P48356-1; Sequence=Displayed; Name=A; IsoId=P48356-2; Sequence=VSP_001697, VSP_001698; Name=C; IsoId=P48356-3; Sequence=VSP_001699, VSP_001700; Name=D; IsoId=P48356-4; Sequence=VSP_001701, VSP_001702; Name=E; IsoId=P48356-5; Sequence=VSP_001703, VSP_001704;

CC -!- TISSUE SPECIFICITY: Isoform A: highest level of expression in lung and kidney, also present in kidney, heart, brain, spleen, liver, muscle, choroid plexus and hypothalamus. Isoform B: highest level of expression in hypothalamus and lower level in brain, testes and adipose tissue. Isoform E: expressed in adipose tissue, hypothalamus, heart, and testes.

CC -!- PTM: Phosphorylated on two tyrosine residues. Tyr-985 may be the major site of phosphorylation. Phosphorylation on both sites is required for full activity.

CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors. Subfamily 2.

CC -!- SIMILARITY: Contains 3 fibronectin type III domains.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

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DR EMBL; U42467; AAC93014.1; -

DR EMBL; U46135; AAC52408.1; -

DR EMBL; U49106; AAC52420.1; -

DR EMBL; U49107; AAC52421.1; -

DR EMBL; U49108; AAC52422.1; -

DR EMBL; U49109; AAC52423.1; -

DR EMBL; U49110; AAC52424.1; -

DR EMBL; U52915; AAC52599.1; -

DR EMBL; Y10298; CAA71343.1; -

DR EMBL; U58861; AAC52705.1; -

DR EMBL; U58862; AAC52706.1; -

DR EMBL; U58863; AAC52707.1; -

DR EMBL; AF039456; AAB95334.1; -

DR EMBL; AF039443; AAB95334.1; JOINED.

DR EMBL; AF039444; AAB95334.1; JOINED.

DR EMBL; AF039445; AAB95334.1; JOINED.

DR EMBL; AF039446; AAB95334.1; JOINED.

DR EMBL; AF039447; AAB95334.1; JOINED.

DR EMBL; AF039448; AAB95334.1; JOINED.

DR EMBL; AF039449; AAB95334.1; JOINED.

DR EMBL; AF039450; AAB95334.1; JOINED.

DR EMBL; AF039451; AAB95334.1; JOINED.

DR EMBL; AF039452; AAB95334.1; JOINED.

DR EMBL; AF039453; AAB95334.1; JOINED.

DR EMBL; AF039454; AAB95334.1; JOINED.

DR EMBL; AF039455; AAB95334.1; JOINED.

DR EMBL; AF039461; AAB95333.1; ALT TERM.

DR EMBL; AF039443; AAB95333.1; JOINED.

DR EMBL; AF039444; AAB95333.1; JOINED.

DR EMBL; AF039445; AAB95333.1; JOINED.

DR EMBL; AF039446; AAB95333.1; JOINED.

DR EMBL; AF039447; AAB95333.1; JOINED.

DR EMBL; AF039448; AAB95333.1; JOINED.

DR EMBL; AF039449; AAB95333.1; JOINED.

DR EMBL; AF039450; AAB95333.1; JOINED.

DR EMBL; AF039451; AAB95333.1; JOINED.

DR EMBL; AF039452; AAB95333.1; JOINED.

DR EMBL; AF039453; AAB95333.1; JOINED.

DR EMBL; AF039454; AAB95333.1; JOINED.

DR EMBL; AF039455; AAB95333.1; JOINED.

DR EMBL; AF039456; AAB95333.1; JOINED.

DR EMBL; AF039457; AAB95333.1; JOINED.

DR EMBL; AF039458; AAB95333.1; JOINED.

DR EMBL; AF039459; AAB95333.1; JOINED.

DR EMBL; AF039459; AAB95335.1; -

DR EMBL; AF039443; AAB95335.1; JOINED.

DR EMBL; AF039444; AAB95335.1; JOINED.

DR EMBL; AF039445; AAB95335.1; JOINED.

DR EMBL; AF039446; AAB95335.1; JOINED.

DR EMBL; AF039447; AAB95335.1; JOINED.

DR EMBL; AF039448; AAB95335.1; JOINED.

DR EMBL; AF039449; AAB95335.1; JOINED.
 DR EMBL; AF039450; AAB95335.1; JOINED.
 DR EMBL; AF039451; AAB95335.1; JOINED.
 DR EMBL; AF039452; AAB95335.1; JOINED.
 DR EMBL; AF039453; AAB95335.1; JOINED.
 DR EMBL; AF039454; AAB95335.1; JOINED.
 DR EMBL; AF039455; AAB95335.1; JOINED.
 DR EMBL; AF039456; AAB95335.1; JOINED.

Query Match 12.1%; Score 144; DB 1; Length 1162;
 Best Local Similarity 31.1%; Pred. No. 0.00011;
 Matches 57; Conservative 22; Mismatches 60; Indels 44; Gaps 11;
 39 LKDE-----ATSCSLHSAHNAHATYTCHEMDFH-----FMADDFSVNITDQSGNYS 87
 177 LKDSPTQVQCNSLRGC-----ECHVFPRAKNYALLWLEITSAGVSFQSLMS 227
 88 QECGSLLAESIKPAPP--FNVVTFSCQYNISWRSYEDPAFVNLKGLQYELQYRNRG 145
 228 LQ--PMLV---VKPDPPGLHMEVTDGKLSQDQMAFF-----PLQYQVKYLENS 276
 146 DPWAYSPRKLSVDSRSV-SLLPLFRKDSYELQVRAGMPGSSYQGTWSEMSDPVIF 204
 277 T--IVREAARIVSATSLVDSVLP-----GSSYEVQVRSKELDGS---GVWSDSSPQVF 326
 205 QTK 207
 327 TTQ 329

RESULT 6

IL2B_MOUSE
 ID IL2B_MOUSE STANDARD; PRT; 539 AA.
 AC P16297;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Interleukin-2 receptor beta chain precursor (IL-2 receptor) (P70-75)
 DE (High affinity IL-2 receptor beta subunit) (CD122).
 GN IL2RB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90175385; PubMed=2155425;
 RA Kono T., Doi T., Yamada G., Hatakeyama M., Minamoto S., Tsudo M.,
 RA Miyasaka M., Miyata T., Taniguchi T.;
 RT "Murine interleukin 2 receptor beta chain: dysregulated gene
 expression in lymphoma line EL-4 caused by a promoter insertion.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:1806-1810(1990).
 CC !- FUNCTION: Receptor for interleukin 2. This beta subunit is
 CC involved in receptor mediated endocytosis and transduces the
 CC mitogenic signals of IL2.
 CC !- SUBUNIT: Noncovalent dimer of an alpha and a beta chains. IL2R
 CC exists in 3 different forms: a high affinity dimer, an
 CC intermediate affinity monomer (beta chain), and a low affinity
 CC monomer (alpha chain). The high and intermediate affinity forms
 CC also associate with a gamma chain.
 CC !- SUBCELLULAR LOCATION: Type I membrane protein.
 CC !- SIMILARITY: Belongs to the type I cytokine family of receptors.
 CC Subfamily 4.

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 or send an email to license@isb-sib.ch).

DR EMBL; M28052; AAA39283.1; ..

DR PIR; A35052; A35052.
 DR HSSP; P14784; IILM.
 DR MCD; MGI:98550; I12rb.
 DR InterPro; IPR002996; CRIA.
 DR InterPro; IPR008957; FN III-like.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR003531; Hemtopoptn_s_F1.
 DR Pfam; PF00041; Fn3; 1.
 DR SMART; SM0060; FN3; 1.
 DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
 KW Receptor; transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 539 INTERLEUKIN-2 RECEPTOR BETA CHAIN.
 FT DOMAIN 27 240 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 241 268 POTENTIAL.
 FT DOMAIN 269 539 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 36 46 BY SIMILARITY.
 FT DISULFID 74 86 BY SIMILARITY.
 FT CARBOHYD 30 30 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 43 43 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 55 55 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 71 71 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 150 150 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 216 216 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 539 AA; 60538 MW; 365C9D206E86FE14 CRC64;

Query Match 11.8%; Score 141.5; DB 1; Length 539;
 Best Local Similarity 22.5%; Pred. No. 6.8e-05;
 Matches 54; Conservative 43; Mismatches 86; Indels 57; Gaps 12;

QY 1 CPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDYELKDEATSCSLHSAHNAHATY 60
 DB 31 CSHLECFYNSRANVSC---MWS-HEEALNV-----TTCVHAKS-NLRHWNK 72
 QY 61 TCHMDVFH-----FMADDFSVNIT--DOSGNYSCGCSFLLAESIK 100
 DB 73 TCELTIVROASWACNLILGSPESQSLTSVLLDINVCWEKGRVVKTCDFHFDNLR 132
 QY 101 PAPPFNVTYTF--SQYINISWR---SDYEPAPFVNLKGLQYELQYRNRGDPVAVSPRR 154
 DB 133 LVAPSLQVLTHTDTCRNMISKVSQVSHYTF-----YLEFARRLLGSHWEDA--- 182
 QY 155 KLISVDSRSVSLPLLEFRKDSYELQVRAGMPGSSYQGTWSEMSDPVIFOTQ-SEELKE 213
 DB 183 SVLSLKQKQWLFLEMLIPSTSYEVQVRAKQRNT--GTWSPMSQPLTFRTPADPMKE 240

RESULT 7

TPOR_HUMAN
 ID TPOR_HUMAN STANDARD; PRT; 635 AA.
 AC P40238;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Thrombopoietin receptor precursor (TPO-R) (Myeloproliferative leukemia
 DE protein) (C-mpl) (CD110 antigen).
 GN MPL OR TPOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=92302297; PubMed=1608974;
 RA Vigon I., Mornon J.-P., Cocault L., Mitjavila M.-T., Tambourin P.,
 RA Gisselbrecht S., Souvri M.;
 RT "Molecular cloning and characterization of MPL, the human homolog of
 RT the v-mpl oncogene: identification of a member of the hematopoietic
 RT growth factor receptor superfamily.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:5640-5644(1992).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=94292186; PubMed=8020956;

RA Mignotte V., Vigon I., Boucher de Crevecoeur E., Romeo P.-H.,
RA Lemarchandel V., Chretien S.;
RT "Structure and transcription of the human c-mpl gene (MPL).";
RL Genomics 20:5-12(1994).
[3]
RP VARIANTS VAL-58 AND LYS-168.
RX MEDLINE=9318093; PubMed=10391209;
RA Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
RA Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nemesh J., Ziaugra L.,
RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
RA Lander E.S.;
RT "Characterization of single-nucleotide polymorphisms in coding regions
of human genes.";
RL Nat. Genet. 22:231-238(1999).
[4]
RP ERRATUM.
RA Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
RA Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nemesh J., Ziaugra L.,
RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
RA Lander E.S.;
RL Nat. Genet. 23:373-373(1999).
CC -!- FUNCTION: Receptor for thrombopoietin. May represent a regulatory
molecule specific for TPO-R-dependent immune responses.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=1; Synonyms=C-mpl-P;
Name=2; Synonyms=C-mpl-K;
IsoId=P40238-1; Sequence=Displayed;
IsoId=P40238-2; Sequence=VSP 001734, VSP 001735;
CC -!- TISSUE SPECIFICITY: Expressed at a low level in a large number of
cells of hematopoietic origin. The two isoforms are always found
to be coexpressed.
CC -!- DISEASE: Defects in MPL are a cause of congenital megakaryocytic
thrombocytopenia (CAMT) [MIM:604498]. CAMT is a disease
characterized by isolated thrombocytopenia and megakaryocytopenia
with no physical anomalies.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
Subfamily 1.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC -!- CAUTION: It is uncertain whether Met-1 or Met-8 is the initiator.
CC -!- DATABASE: NAME=PROW; NOTE=PROW 1:22-25(2000).
WWW="http://www.ncbi.nlm.nih.gov/prow/guide/11586825_g.htm".

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EMBL; M90102; AAA69971.1; -
EMBL; M90103; AAA69972.1; -
EMBL; U68162; AAB08424.1; -
EMBL; U68159; AAB08424.1; JOINED.
EMBL; U68160; AAB08424.1; JOINED.
EMBL; U68161; AAB08424.1; JOINED.
EMBL; U68162; AAB08425.1; -
EMBL; U68159; AAB08425.1; JOINED.
EMBL; U68160; AAB08425.1; JOINED.
EMBL; U68161; AAB08425.1; JOINED.
EMBL; U68162; AAB08425.1; JOINED.
PIR; A45266; A45266.
PIR; B45266; B45266.
HSPSP; P12325; 1EBA.
Genew; HGNC:721; MPL.
MIM; 159530; -
MIM; 604498; -
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0004888; F:transmembrane receptor activity; TAS.
GO; GO:0008283; P:cell proliferation; TAS.
GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
InterPro; IPR002996; CR1A.

DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003528; Hemtopoptn_L_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01352; HEMATOPO. REC L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing;
Repeat; Antigen; Polymorphism.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 635 THROMBOPOIETIN RECEPTOR.
FT DOMAIN 26 491 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 492 513 POTENTIAL.
FT DOMAIN 514 635 CYTOPLASMIC (POTENTIAL).
FT DISULFID 40 50 BY SIMILARITY.
FT DISULFID 77 93 BY SIMILARITY.
FT DISULFID 291 301 BY SIMILARITY.
FT DISULFID 323 334 BY SIMILARITY.
FT CARBOHYD 117 117 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 298 298 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 358 358 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPLIC 523 579 RLRHLPSPDLHRLVGLGYLDTAALSPPKATVSDTCEEV
EPSLLEILPKSSRTPT -> YRPROAGDWRTWRWSRTCKQA
FLVRSVTPDLRPPPTVRYTGFPALPARHLWDSPLRLTL (in
isoform 2).
FT VARSPLIC 580 635 /FTid=VSP_001734.
Missing (in isoform 2).
FT VARIANT 58 58 /FTid=VSP_001735.
A -> V (in dbSNP:6087).
FT VARIANT 168 168 /FTid=VAR_011988.
E -> K (in dbSNP:6088).
/FTid=VAR_011989.
SQ SEQUENCE 635 AA; 71244 MW; D25D8D8959359DDC CRC64;
Query Match 11.6%; Score 139; DB 1; Length 635;
Best Local Similarity 24.0%; Pred. No. 0.00014;
Matches 59; Conservative 25; Mismatches 76; Indels 86; Gaps 14;
QY 4 LVCTDYDTQTVICILEMMNLHPSLTITLTPQDYBELKDEATCSL--HRSAHNATHATY- 60
DB 289 LQCFTLDLKNVTC-----QWQQQ-----DHASSQGFYHSHRACCPDRYP 329
QY 61 -----TCHM-----DVHFMADDIFSVNITDSQSNYSCECS-F 93
DB 330 TWNECEEKNTNGLQTPQFRCFKGRNDSIIHL-----VEVTAPGVTHYLSGPF 383
QY 94 LIAESIK-PAPPFNVTVTFSGQYNISWRSDYEDPAFYMLKGLQYELQYRNRG-DPWAVS 151
DB 384 WTHQAVRLPTNLHWRETSSGHLEW----QHPSSWAAQ-ETCYQLRYTGEHQDKV- 437
QY 152 PARKLISVDSRSVSLP-----LEFRKDSYELQVRAGPMGSSYQGTWSEWSDPI 203
DB 438 -----LEPPLGARGGTLELRPSRYLQRA-RLNGPTYQGFWSSWDPT 482
QY 204 FOTOSE 209
DB 483 VETATE 488
RESULT 8
LEPR RAT
ID LEPR RAT STANDARD; PRT; 1162 AA.
AC Q62959; Q62959; Q54805; P70493; P70494; P70495; P97589;
AC Q62960; Q63007; Q63385; Q63386; Q9ER14;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Leptin receptor precursor (LEP-R) (OB receptor) (OB-R).
GN LEPR OR OBR OR FA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

RN RP SEQUENCE FROM N.A. (ISOFORM B), AND VARIANT FA PRO-269.
RC STRAIN=Zucker; TISSUE=Hypothalamus;
RX MEDLINE=96241565; PubMed=8673096;
RA Phillips M.S., Liu Q., Hammond H.A., Dugan V., Hey P.J., Caskey C.T.,
Hess J.F.;
RT "Leptin receptor missense mutation in the fatty Zucker rat.";
RL Nat. Genet. 13:18-19(1996).
[2]
RN RP SEQUENCE FROM N.A. (ISOFORM B), AND VARIANT FA PRO-269.
RC STRAIN=Sprague-Dawley, and Zucker fatty; TISSUE=Brain;
RX MEDLINE=96295531; PubMed=8702432;
RA Iida M., Murakami T., Ishida K., Mizuno A., Kuwajima M., Shima K.;
RT "Substitution at codon 269 (Glutamine --> proline) of the leptin
receptor (OB-R) cDNA is the only mutation found in the Zucker fatty
(fa/fa) rat.";
RL Biochem. Biophys. Res. Commun. 224:597-604(1996).
[3]
RN RP SEQUENCE FROM N.A. (ISOFORMS A; B AND E), AND VARIANT FA PRO-269.
RC STRAIN=Sprague-Dawley, and Zucker fatty;
RX MEDLINE=96332408; PubMed=8769097;
RA Takaya K., Ogawa Y., Isse N., Okazaki T., Satoh N., Masuzaki H.,
Mori K., Tamura N., Hosoda K., Nakao K.;
RT "Molecular cloning of rat leptin receptor isoform complementary
DNAs -- identification of a missense mutation in Zucker fatty (fa/fa)
rats.";
RL Biochem. Biophys. Res. Commun. 225:75-83(1996).
[4]
RN RP SEQUENCE FROM N.A. (ISOFORM B).
RA Karlsson C., Lindell K., Robinson I.C.A.F., Carlsson L.M.S.,
Carlsson B.;
RT "Cloning of the rat leptin receptor.";
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
[5]
RN RP SEQUENCE FROM N.A. (ISOFORM A), AND VARIANT FA PRO-269.
RC STRAIN=Sprague-Dawley, and Zucker fatty;
RX MEDLINE=96212906; PubMed=8630068;
RA Iida M., Murakami T., Ishida K., Mizuno A., Kuwajima M., Shima K.;
RT "Phenotype-linked amino acid alteration in leptin receptor cDNA from
Zucker fatty (fa/fa) rat.";
RL Biochem. Biophys. Res. Commun. 222:19-26(1996).
[6]
RN RP SEQUENCE FROM N.A. (ISOFORM B).
RC STRAIN=Sprague-Dawley; TISSUE=Spleen;
RA Park J.H., Ju S.K., Na S.Y., You K.H., Kim K.L.;
RT "Molecular cloning, sequencing, and recombinant expression of the long
form of the rat leptin receptor isolated from whole spleen RNA.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
[7]
RN RP SEQUENCE FROM N.A. (ISOFORM F).
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=96368027; PubMed=8772180;
RA Wang M.-Y., Zhou Y.T., Newgard C.B., Unger R.H.;
RT "A novel leptin receptor isoform in rat.";
RL FEBS Lett. 392:87-90(1996).
[8]
RN RP SEQUENCE OF 1-123 FROM N.A.
RA Morishita T., Hida T., Kuzuyama T., Noguchi T.;
RT "Analysis of rat leptin receptor gene.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
[9]
RN RP SEQUENCE OF 557-802 AND 843-892 FROM N.A. (ISOFORMS C AND E).
RC STRAIN=Sprague-Dawley;
RX MEDLINE=97415825; PubMed=9268737;
RA Chien E.K., Hara M., Rouard M., Yano H., Phillippe M., Polonsky K.S.,
Bell G.I.;
RT "Increase in serum leptin and uterine leptin receptor messenger RNA
levels during pregnancy in rats.";
RL Biochem. Biophys. Res. Commun. 237:476-480(1997).
[10]
RN RP SEQUENCE OF 694-878 FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Pancreas;
RA Ma Z.;
RT "Identification of a leptin receptor in islet.";
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
[11]
RN RP SEQUENCE OF 821-894 FROM N.A. (ISOFORM A).
RC STRAIN=Wistar Munich; TISSUE=Kidney;
RA Totsune K., Takanashi K., Mackenzie H.S., Murakami O., Arihara Z.,
Sone M., Satoh F., Mouril T., Brenner B.W., Ito S.;
RT "Leptin receptor gene expression in rat kidney.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
[12]
RN RP VARIANT FA PRO-269.
RX MEDLINE=96314329; PubMed=8690163;
RA Chua S.C. Jr., White D.W., Wu-Peng X.S., Liu S.M., Okada N.,
Kerslaw E.B., Chung W.K., Power-Kehoe L., Chua M., Tartaglia L.A.,
Leibel R.L.;
RT "Phenotype of fatty due to Glr269Pro mutation in the leptin receptor
(Lepr).";
RL Diabetes 45:1141-1143(1996).
CC -!- FUNCTION: Receptor for obesity factor (leptin). Involved in the
regulation of fat metabolism and in a hematopoietic pathway
required for normal lymphopoiesis. May play a role in
reproduction.
CC -!- FUNCTION: The short form (isoform A) may act to transport leptin
to the cerebrospinal fluid. The putative soluble receptor (isoform
B) could function as a transport protein.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Except for form E
which could be secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=6;
CC Name=B;
CC ISOID=Q62959-1; Sequence=Displayed;
CC Name=A;
CC ISOID=Q62959-2; Sequence=VSP_001705, VSP_001706;
CC Name=C;
CC ISOID=Q62959-3; Sequence=VSP_001707, VSP_001708;
CC Name=D;
CC ISOID=Q62959-6; Sequence=Not described;
CC Name=E;
CC ISOID=Q62959-4; Sequence=VSP_001709, VSP_001710;
CC Name=F;
CC ISOID=Q62959-5; Sequence=VSP_001711, VSP_001712;
CC -!- TISSUE SPECIFICITY: Isoform B is expressed in kidney, liver, lung,
ovary, spleen and uterus. Increased level in uterus during
gestation. Isoform F is expressed at high levels in liver and
spleen and less in brain, stomach, kidney, thymus, heart, lung and
hypothalamus.
CC -!- PTM: Phosphorylated on two tyrosine residues. Tyr-985 may be the
major site of phosphorylation. Phosphorylation on both sites is
required for full activity (By similarity).
CC -!- DISEASE: The fatty (FA) mutation produces profound obesity of
early onset caused by hyperphagia, defective nonshivering
thermogenesis, and preferential deposition of energy into adipose
tissue.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
Subfamily 2.
CC -!- SIMILARITY: Contains 3 fibronectin type III domains.
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or send an email to license@sib-sib.ch).

DR EMBL: AF287258; AAF89300.1; --
 DR EMBL: U53144; AAB03088.1; --
 DR EMBL: D84126; BAA12231.1; --
 DR EMBL: AB011006; BAA24899.1; --
 DR EMBL: AF007818; AAB63201.1; --
 DR EMBL: AF007819; AAB63202.1; --
 DR EMBL: U67207; AAB40654.1; --
 DR EMBL: AF304191; AAG22823.1; --
 DR InterPro: IPR002996; CRA.
 DR InterPro: IPR008957; FN III-like.
 DR InterPro: IPR003961; FN III.
 DR InterPro: IPR003529; Hemtopoptn_L_F2.
 DR Pfam: PF00041; fn3; 2.
 DR PROSITE: PS01353; HEMATOPO REC L_F2; 1.
 KW Obesity; Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
 KW Alternative splicing; Phosphorylation; Polymorphism.
 FT CHAIN 1 21
 FT SIGNAL 22 1162
 FT DOMAIN 22 839
 FT TRANSMEM 840 860
 FT DOMAIN 861 1162
 FT CYTOPLASMIC (POTENTIAL).
 FT FIBRONECTIN TYPE-III 1.
 FT FIBRONECTIN TYPE-III 2.
 FT FIBRONECTIN TYPE-III 3.
 FT DOMAIN 736 821
 FT BY SIMILARITY.
 FT DISULFID 737 90
 FT BY SIMILARITY.
 FT DISULFID 89 99
 FT BY SIMILARITY.
 FT DISULFID 131 142
 FT BY SIMILARITY.
 FT DISULFID 186 195
 FT BY SIMILARITY.
 FT DISULFID 188 193
 FT BY SIMILARITY.
 FT DISULFID 350 410
 FT BY SIMILARITY.
 FT DISULFID 411 416
 FT BY SIMILARITY.
 FT DISULFID 471 526
 FT BY SIMILARITY.
 FT DISULFID 486 496
 FT BY SIMILARITY.
 FT CARBOHYD 55 55
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 56 56
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 73 73
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 98 98
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 187 187
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 275 275
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 345 345
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 356 356
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 431 431
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 Query Match 11.5%; Score 138; DB 1; Length 1162;
 Best Local Similarity 30.9%; Pred. No. 0.00036;
 Matches 56; Conservative 23; Mismatches 62; Indels 40; Gaps 11;
 2y 39 LKD--EATSCSLHRSANATHATVTCMDVFFH-----FMADDIFSVNITDQSGNYSOE 89
 177 LKDSFQTVQC-----NCSVRECECHVPVPRAKVYVALLMYLEITSAGVSFQSLMSLQ 229
 2y 90 CGSELLAESIKAPP--FNVTVTFSGQYNISWRSDYEDPAPYMLKGKLYELQYRNGDP 147
 230 --PMLV---VKPDPLGLRMEVTDGGLKISWDSQTKAPF-----PLQVQVYLENST- 277
 2y 148 WAYSPEKRLSVDSRSV-SLLPLEFRKDSSELQVVRAGMPGSSYOGTWSWSDPVIFOT 206
 278 -IVREAAEIVSDTSLLDVSLP-----GSSIEVQVRSKRDLGS---GVWSDMSLPOLFTT 328
 2y 207 Q 207
 2y 329 Q 329
 RESULT 9
 LEPR HUMAN STANDARD; PRT; 1165 AA.
 AC P48357; Q13592; Q13593; Q13594; Q92919; Q92920; Q92921;
 JT 01-FEB-1996 (Rel. 33, Created)
 JT 01-FEB-1996 (Rel. 33, Last sequence update)
 JT 15-MAR-2004 (Rel. 43, Last annotation update)
 28 Leptin receptor precursor (Lepr-R) (OB-R) (Hub219).
 3N LEPR OR OBR OR DB.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1] _SEQUENCE FROM N.A. (ISOFORMS B AND E).
 RC TISSUE=Brain;
 RX MEDLINE=96128129; PubMed=8548812;
 RA Tartaglia L.A., Dembski M., Wang X., Deng N., Culpepper J.,
 RA Devos R., Richards G.J., Campfield L.A., Clark F.T., Deeds J.,
 RA Muir C., Sanker S., Moriarty A., Moore K.J., Smutko J.S.,
 RA Mays G.G., Wolf E.A., Monroe C.A., Tepper R.I.;
 RT "Identification and expression cloning of a leptin receptor, OB-R.";
 RL Cell 83:1263-1271(1995).
 RN [2]
 RC SEQUENCE FROM N.A. (ISOFORMS A; B AND C).
 RX TISSUE=Fetal liver;
 RX MEDLINE=96398968; PubMed=8805376;
 RA Bennett B.D., Solar G.P., Yuan J.Q., Mathias J., Thomas G.R.,
 RA Matthews W.;
 RT "A role for leptin and its cognate receptor in hematopoiesis.";
 RL Curr. Biol. 6:1170-1180(1996).
 RN [3]
 RC SEQUENCE FROM N.A. (ISOFORM B), AND VARIANTS ARG-109 AND ARG-223.
 RX MEDLINE=97301763; PubMed=9158141;
 RA Thompson D.B., Ravussin E., Bennett P.H., Bogardus C.;
 RT "Structure and sequence variation at the human leptin receptor gene in
 RL lean and obese Pima Indians.";
 RL Hum. Mol. Genet. 6:675-679(1997).
 RN [4]
 RC SEQUENCE FROM N.A. (ISOFORM A).
 RX MEDLINE=97215244; PubMed=9061609;
 RA Luch S.-M., Di Marco F., Levin N., Armanini M., Xie M.H., Nelson C.,
 RA Bennett G.L., Williams M., Spencer S.A., Gurney A., de Sauvage P.J.;
 RT "Cloning and characterization of a human leptin receptor using a
 RL biologically active leptin immunoadhesin.";
 RL J. Mol. Endocrinol. 18:77-85(1997).
 RN [5]
 RC SEQUENCE FROM N.A. (ISOFORMS A; C AND D).
 RX TISSUE=Fetal liver;
 RX MEDLINE=96206286; PubMed=8616721;
 RA Cioffi J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J., Mikhail A.,
 RA Platika D., Shodgrass H.R.;
 RT "Novel B219/OB receptor isoforms: possible role of leptin in
 RL hematopoiesis and reproduction.";
 RL Nat. Med. 2:585-589(1996).
 RN [6]
 RC ALTERNATIVE SPLICING DUE TO AN ENDOGENOUS RETROVIRUS.
 RX MEDLINE=99128223; PubMed=9929394;
 RA Kapitonov V.V., Jurka J.;
 RT "The long terminal repeat of an endogenous retrovirus induces
 RT alternative splicing and encodes an additional carboxy-terminal
 RT sequence in the human leptin receptor.";
 RL J. Mol. Evol. 48:248-251(1999).
 RN [7]
 RC CARBOHYDRATE-LINKAGE SITES, DISULFIDE BONDS, AND PARTIAL SEQUENCE.
 RX MEDLINE=99003211; PubMed=9786864;
 RA Hanlu M., Arakawa T., Bures E.J., Young Y., Hui J.O., Rohde M.F.,
 RA Welcher A.A., Horan T.;
 RT "Human leptin receptor. Determination of disulfide structure and
 RT N-glycosylation sites of the extracellular domain.";
 RL J. Biol. Chem. 273:28691-28695(1998).
 RN [8]
 RC VARIANT ARG-223.
 RX MEDLINE=96270489; PubMed=8666155;
 RA Considine R.V., Considine E.L., Williams C.J., Hyde T.M., Caro J.F.;
 RT "The hypothalamic leptin receptor in humans: identification of
 RT incidental sequence polymorphisms and absence of the db/db mouse and
 RL fa/fa rat mutations.";
 RL Diabetes 45:992-994(1996).
 RN [9]
 RC VARIANTS ARG-109; ARG-204; ARG-223 AND ASN-656.
 RX MEDLINE=97289527; PubMed=9144432;

RA Schwald S.M., Soerensen T.D., Soerensen T.I., Tybjaerg-Hansen A.,
RA Andersen T., Chung W.K., Leibel R.L., Pedersen O.;
RT "Amino acid variants in the human leptin receptor: lack of association
to juvenile onset obesity.";
RL Biochem. Biophys. Res. Commun. 233:248-252(1997).
RN [10]
RP VARIANTS ARG-109; ARG-223 AND ASN-656.
RX MEDLINE=97431549; PubMed=9287054;
RA Chung W.K., Power-Keoh L., Chua M., Chu F., Azone L., Huma Z.,
RA Sothorn M., Udall J.N., Kahle B., Leibel R.L.;
RT "Exonic and intronic sequence variation in the human leptin receptor
gene (LEPR).";
RL Diabetes 46:1509-1511(1997).
RN [11]
RP VARIANTS ARG-109; ARG-223; ASN-656 AND THR-675.
RX MEDLINE=97075638; PubMed=9860295;
RA Roth H., Korn T., Rosenkranz K., Hinney A., Ziegler A., Kunz J.,
RA Siegfried W., Mayer H., Hebebrand J., Grzeschik K.-H.;
RT "Transmission disequilibrium and sequence variants at the leptin
receptor gene in extremely obese German children and adolescents.";
RL Hum. Genet. 103:540-546(1998).
RN [12]
RP VARIANTS ARG-109; ARG-223 AND ASN-656.
RX MEDLINE=97318795; PubMed=9175732;
RA Gotoda T., Manning B.S., Goldstone A.P., Imrie H., Evans A.L.,
RA Strosberg A.D., McKeigue P.M., Scott J., Altman T.J.;
RT "Leptin receptor gene variation and obesity: lack of association in a
white British male population.";
RL Hum. Mol. Genet. 6:869-876(1997).
CC -!- FUNCTION: Receptor for obesity factor (leptin). Involved in the
regulation of fat metabolism and in a hematopoietic pathway
required for normal lymphopoiesis. May play a role in
reproduction.
CC -!- FUNCTION: The short form (isoform A) may act to transport leptin
to the cerebrospinal fluid (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Except for form B
which could be soluble.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=5;
CC Name=A; Synonyms=13.2, OBRb;
CC IsoId=P48357-1; SequencesDisplayed;
CC Name=A; Synonyms=6.4, HuB219.3;
CC IsoId=P48357-2; Sequences=VSP_001689, VSP_001690;
CC Name=C; Synonyms=12.1, OBRa;
CC IsoId=P48357-3; Sequences=VSP_001691, VSP_001692;
CC Name=D; Synonyms=HuB219.2;
CC IsoId=P48357-4; Sequences=VSP_001693, VSP_001694;
CC Name=E;
CC IsoId=P48357-5; Sequences=VSP_001688;
CC -!- TISSUE SPECIFICITY: Isoform A expressed in fetal liver and in
hematopoietic tissues and choroid plexus. In adults highest
expression in lung, liver, small intestine, prostate and ovary.
CC Low level in heart and kidney. Isoform B is highly expressed in
hypothalamus.
CC -!- DOMAIN: The cytoplasmic domain may be essential for intracellular
signal transduction by activation of JAK tyrosine kinase and
STATs.
CC -!- PTM: Phosphorylated on two tyrosine residues. Tyr-986 may be the
major site of phosphorylation. Phosphorylation on both sites is
required for full activity (By similarity).
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC -!- Subfamily 2.
CC -!- SIMILARITY: Contains 3 fibronectin type III domains.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

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the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).

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DE antigen).
DN IL4R OR IL4RA OR 582J2.1.
DS Homo sapiens (Human).
DC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
DX NCBI_TaxID=9606;
DX [1]
XP SEQUENCE FROM N.A.
XC TISSUE=Peripheral blood;
XX MEDLINE=90171849; PubMed=2307934;
RA Idzerda R.L., March C.J., Mosley B., Lyman S.D., Bos T.V.,
RA Gimpel S.D., Din W.S., Grabstein K.H., Widmer M.B., Park L.S.,
RA Cosman D., Beckmann M.P.;
RA "Human interleukin 4 receptor confers biological responsiveness and
RT defines a novel receptor superfamily.";
XL J. Exp. Med. 171:861-873(1990).
RN [2]
RN SEQUENCE FROM N.A.
RP MEDLINE=91120547; PubMed=278997;
RA Galizzi J.-P., Zuber C.E., Harada N., Gorman D.M., Djossou O.,
RA Kastelein R., Banchereau J., Howard M., Miyajima A.;
RA "Molecular cloning of a cDNA encoding the human interleukin 4
RT receptor.";
XL Int. Immunol. 2:669-675(1990).
RN [3]
RN SEQUENCE FROM N.A.
RP MEDLINE=9245270; PubMed=10493829;
RA Loftus B.J., Kim U.-J., Sredon V.P., Kalush F., Brandon R.,
RA Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,
RA Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,
RA Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;
RA "Genome duplications and other features in 12 Mb of DNA sequence from
RT human chromosome 16p and 16q.";
XL Genomics 60:295-308(1999).
RN [4]
RN SEQUENCE FROM N.A.
RP Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RA Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RN VARIANTS VAL-75; ALA-400; ARG-431; LEU-436 AND PRO-786.
XX MEDLINE=97224413; PubMed=9070874;
RA Deichmann K., Bardutzky J., Forster J., Heinzmann A., Kuehr J.;
RA "Common polymorphisms in the coding part of the IL4-receptor gene.";
XL Biochem. Biophys. Res. Commun. 231:696-697(1997).
RN [6]
RN VARIANT ATOPIC ARG-576.
XX MEDLINE=98041803; PubMed=9392697;
RA Hershey G.K.K., Friedrich M.F., Esswein L.A., Thomas M.L.,
RA Chatila T.A.;
RA "The association of atopy with a gain-of-function mutation in the
RT alpha subunit of the interleukin-4 receptor.";
XL New Engl. J. Med. 337:1720-1725(1997).
RN [7]
RN VARIANT ATOPIC ASTHMA VAL-75.
XX MEDLINE=98282087; PubMed=9620765;
RA Mitsuyasu H., Izuura K., Mao X.-Q., Gao P.S., Arinobu Y., Enomoto T.,
RA Kawai M., Sasaki S., Dake Y., Hamasaki N., Shirakawa T., Hopkin J.M.;
RA "Ile50Val variant of IL4R alpha upregulates IgE synthesis and
RT associates with atopic asthma.";
XL Nat. Genet. 19:119-120(1998).
RN [8]
RN VARIANT ATOPIC ASTHMA VAL-75.
XX MEDLINE=99322293; PubMed=10390422;
RA Noguchi E., Shibasaki M., Arinami T., Takeda K., Yokouchi Y.,
RA Kobayashi K., Imoto N., Nakahara S., Matsui A., Hamaguchi H.;
RA "No association between atopy/asthma and the Ile50Val polymorphism of
RT IL-4 receptor.";
XL Am. J. Respir. Crit. Care Med. 160:342-345(1999).
RN [9]
RN VARIANTS PRO-503 AND ARG-576.
XX MEDLINE=99250314; PubMed=10233717;
RA Kruse S., Japha T., Tedner M., Sparholt S.H., Forster J., Kuehr J.,
RA

RA Delchmann K.A.;
RT "The polymorphisms S503P and Q576R in the interleukin-4 receptor alpha
RT gene are associated with atopy and influence the signal
RT transduction.";
RN Immunology 96:365-371(1999).
RN [10]
RN VARIANT ALA-752.
RX MEDLINE=20143377; PubMed=10677312;
RA Ober C., Leavitt S.A., Tsalenko A., Howard T.D., Hoki D.M., Daniel R.,
RA Newman D.L., Wu X., Parry R., Lester L.A., Solway J., Blumenthal M.,
RA King R.A., Xu J., Meyers D.A., Bleeker E.R., Cox N.J.;
RA "Variation in the interleukin 4-receptor alpha gene confers
RT susceptibility to asthma and atopy in ethnically diverse
RT populations.";
XL Am. J. Hum. Genet. 66:517-526(2000).
RN [11]
RN VARIANT ATOPIC DERMATITIS ARG-576.
RX MEDLINE=20269830; PubMed=10809862;
RA Oiso N., Fukai K., Ishii M.;
RA "Interleukin 4 receptor alpha chain polymorphism Gln551Arg is
RT associated with adult atopic dermatitis in Japan.";
XL Br. J. Dermatol. 142:1003-1006(2000).
RN [12]
RN VARIANT PRO-786.
RX MEDLINE=21405389; PubMed=11513543;
RA Andrews R.P., Burrell L., Rosa-Rosa L., Cunningham C.M.,
RA Brzezinski J.L., Bernstein J.A., Khurana Hershey G.K.;
RA "Analysis of the Ser786Pro interleukin-4 receptor alpha allelic
RT variant in allergic and nonallergic asthma and its functional
RT consequences.";
XL Clin. Immunol. 100:298-304(2001).
RN [13]
RN VARIANT ILE-579.
RX MEDLINE=21182061; PubMed=11285129;
RA Lozano F., Places L., Vila J.M., Padilla O., Arman M., Gimferrer I.,
RA Suarez E., Lopez de la Iglesia A., Miserachs N., Vives J.; (Val554Ile)
RA "Identification of a novel single-nucleotide polymorphism
RT and definition of eight common alleles for human IL4RA exon 11.";
XL Tissue Antigens 57:216-220(2001).
RN CC -!- FUNCTION: This is a receptor for interleukin 4. A soluble form
CC of the IL4 receptor may represent a regulatory molecule specific
CC for IL4-dependent immune responses.
CC -!- SUBUNIT: Heterodimer of an alpha chain and a common gamma chain.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DISEASE: Defects in IL4R are a cause of susceptibility to atopic
CC asthma [MIM:147781].
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC Subfamily 4.
CC -!- DATABASE: NAME=PRO; NOTE=CD guide CD124 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd124.htm".
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; X52425; CAA36672.1; -.
CC EMBL; AC004525; AAC23495.1; -.
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CC PIR; A60386; A60386.
CC PDB; 1IAR; 03-MAR-00.
CC PDB; 1IRS; 15-MAY-97.
CC PDB; 1ITE; 26-JAN-95.
CC Genew; HGNC:6015; IL4R.
CC MIM; 147781; -.
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0004913; P:interleukin-4 receptor activity; TAS.
CC GO; GO:0005057; P:receptor signaling protein activity; TAS.
CC GO; GO:0006935; P:immune response; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.

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DR InterPro: IPR002996; CRIA.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003531; Hemtopoptn_S_F1.
DR SMART: SM00060; FN3; 1.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Disease mutation;
KW Polymorphism; 3D-structure.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 825 INTERLEUKIN-4 RECEPTOR ALPHA CHAIN.
FT DOMAIN 26 232 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 233 256 POTENTIAL.
FT DOMAIN 257 825 CYTOPLASMIC (POTENTIAL).
FT DISULFID 34 44 BY SIMILARITY.
FT DISULFID 74 86 BY SIMILARITY.
FT CARBOHYD 53 53 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 128 128 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 176 176 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 209 209 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT VARIANT 400 400 E -> A (in dbSNP:1805011).
FT VARIANT 431 431 C -> R (in dbSNP:1805012).
FT VARIANT 436 436 S -> L (in dbSNP:1805013).
FT VARIANT 503 503 S -> P (in dbSNP:1805015).
FT VARIANT 576 576 O -> R (in atopic dermatitis;
FT dbSNP:1801275).
FT VARIANT 579 579 V -> I.
FT VARIANT 752 752 S -> A (in dbSNP:1805016).
FT VARIANT 786 786 S -> P (in 1.8% of the population;
FT dbSNP:1805014).
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DB 34 CVSDYMSITC---BWKMGPTNCSTELRLYLQVLF--LLSEAHTC---IPENNGGAGC 84
QY 61 TCHMDVPHFMADDFSVNITDQSGNSDEC-----GSFLAESIKPAPPENVTV-- 109
DB 85 VCHL-----LMDVVVSAD-----NYTDLWAGQQLLWKGSKPSEHVXKPRAPGNLIVHT 133
QY 110 TFGQYINISWSDYEDDPAYMLKGLQYELQVRNGDPWAVSPRRKLISVDVSRVSL 169
DB 134 NVSDTLTLTWSNPF--PPDNLVNLHLYAVNIWSENDP-----ADFRIYNYTYL 180
QY 170 E-----FEKDSGYELOVRAGMPGSSVCGGTWSEWS 199
DB 181 EPLSLIAASTLKSIGSYRVRVAVW---AQCYNTTWSEWS 216
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DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Leptin receptor precursor (LEP-R) (OB-R).
GN LEPR OR OBR.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
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RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
RX MEDLINE=98408931; PubMed=9738551;
RA Hotta K., Gustafson T.A., Ortmeier H.K., Bodkin N.L., Hansen B.C.;
RT "Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA
RT expression in the adipose tissue of normal, hyperinsulinemic, and type
RL 2 diabetic rhesus monkeys.";
RN Obes. Res. 6:353-360(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
RX MEDLINE=98408931; PubMed=9738551;
RA Hotta K., Gustafson T.A., Ortmeier H.K., Bodkin N.L., Hansen B.C.;
RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX Gustafson T.A., Ortmeier H.K., Bodkin N.L., Hansen B.C.;
RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Receptor for obesity factor (leptin). Involved in the
CC regulation of fat metabolism and in a hematopoietic pathway
CC required for normal lymphopoiesis. May play a role in
CC reproduction.
CC -I- FUNCTION: The short form (isoform A) may act to transport leptin
CC to the cerebrospinal fluid (By similarity).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=B;
CC IsoId=Q9MYL0-1; Sequences=Displayed;
CC Name=A;
CC IsoId=Q9MYL0-2; Sequences=VSP 001695; VSP 001696;
CC -I- TISSUE SPECIFICITY: Widely expressed. High expression of isoform B
CC in liver, adipose tissue, hypothalamus and choroid plexus.
CC -I- DOMAIN: The cytoplasmic domain may be essential for intracellular
CC signal transduction by activation of JAK tyrosine kinase and
CC STATs.
CC -I- PTM: Phosphorylated on two tyrosine residues. Tyr-984 may be the
CC major site of phosphorylation. Phosphorylation on both sites is
CC required for full activity (By similarity).
CC -I- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC Subfamily 2.
CC -I- SIMILARITY: Contains 3 fibronectin type III domains.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC EMBL; AF225874; AAF35388.1; -
CC EMBL; AF225875; AAF35389.1; -
CC EMBL; AF225873; AAF35387.1; -
CC EMBL; AF222960; AAF34683.1; -
CC HSSP; P16471; 1BP3.
CC InterPro: IPR002956; CRIA.
CC InterPro: IPR008957; FN_III-like.
CC InterPro: IPR003961; FN_III.
CC InterPro: IPR003529; Hemtopoptn_L_F2.
CC InterPro: IPR003531; Hemtopoptn_S_F1.
CC Pfam; PF00041; fn3; 2.
CC SMART; SM00060; FN3; 4.
CC PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
CC PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
KW Obesity; Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
KW Alternative splicing; Phosphorylation.
FT SIGNAL 1 21 POTENTIAL.

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CC -I- SIMILARITY; Belongs to the type I cytokine family of receptors.  
CC Subfamily 4.  
CC  
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CC  
CC EMBL; M55050; AAA41429.1; -.  
DR HGSP; P14784; IILM.  
DR InterPro; IPR002996; CR1A.  
DR InterPro; IPR008957; FN III-like.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR003531; Hemoptoptn_S_Fl.  
DR SMART; SMO0060; FN3; 1.  
DR PROSITE; PS01355; HEMATOPO REC_S_F1; 1.  
KM Receptor; Transmembrane; Glycoprotein; Signal.  
FT SIGNAL 1 26 POTENTIAL.  
FT CHAIN 27 537 INTERLEUKIN-2 RECEPTOR BETA CHAIN.  
FT DOMAIN 27 239 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 240 267 POTENTIAL.  
FT DOMAIN 268 537 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 36 46 BY SIMILARITY.  
FT DISULFID 74 86 BY SIMILARITY.  
FT CARBOHYD 43 43 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 55 55 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 71 71 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 150 150 N-LINKED (GLCNAC. .) (POTENTIAL).  
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Best Local Similarity 23.1%; Pred.No.0.0003;  
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QY 1 CPDLVCYTQYLQTVICILEMWNLHPSTLTITWQDYEEELKDEA---TSCSLHSAH-----53  
DB 31 CSHLKCFYNRAVNSC---MWS-----PERALNVTSCIHAKSMDRHW 70  
  
QY 54 NAT-----HATYTCHM-----DVFEHMADDIFSVNIT--DOSGNYSQEGCSFLAES 98  
DB 71 NKTCETPVQASNAWNCLILGPLDSQSITSVDLSLVVCWEKGWRVKVCTTFPPDN 130  
  
QY 99 IKDPAPPNVTVTF--SGQYNISWR-----SDYEDPAFYMLKGKLQVELQYLRNGRDPWA VSP 152  
DB 131 LRLIAPHSLQLVLIHIEFRRCNISWEVSQVSHYNP-----YLEPE-----A 170  
  
QY 153 ERKLIQSDRSVSLPLEPK-----DSSYELOVRAGMPGSSYGWTSEWSDPV 202  
DB 171 RRLLRSDSWEDASVFSLKQRQWIFLETTPDTSYELQVRVAQRGT--RTWSPWSPQM 228  
  
QY 203 IFOTOSEELKE 213  
DB 229 AFETRDPADPKE 239  
  
RESULT 13  
CYRG_MOUSE STANDARD; PRT; 369 AA.  
ID CYRG_MOUSE ID AC P34902;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Cytokine receptor common gamma chain precursor (Gamma-C)  
DE (interleukin-2 receptor gamma chain) (IL-2R gamma chain) (P64).  
DR IL2RG.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxId=10090;  
RN [1]
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Q08351;
 01-FEB-1995 (Rel. 31, Created)
 01-FEB-1995 (Rel. 31, Last sequence update)
 15-MAR-2004 (Rel. 43, Last annotation update)
 Thrombopoietin receptor precursor (TPO-R) (Myeloproliferative leukemia protein) (C-mpl).
 3N MPL OR TPOR.
 3S Mus musculus (Mouse).
 3C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 3C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 3X NCBI_TaxID=10090;
 3X [1]
 SEQUENCE FROM N.A.
 RP MEDLINE=93327753; PubMed=8334987;
 RA Skoda R.C., Seldin D.C., Chiang M.K., Peichel C.L., Vogt T.F.,
 RT Leder P.;
 RT "Murine c-mpl: a member of the hematopoietic growth factor receptor
 RT superfamily that transduces a proliferative signal.";
 RL EMBO J. 12:2645-2653(1993).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=ICFW; TISSUE=Fetal liver;
 RX MEDLINE=93390933; PubMed=8397366;
 RA Vigon I., Florindo C., Fitchelson S., Guenet J.-L., Mattei M.-G.,
 RX Souyri M., Cosman D., Gisselbrecht S.;
 RT "Characterization of the murine Mpl proto-oncogene, a member of the
 RT hematopoietic cytokine receptor family: molecular cloning,
 RT chromosomal location and evidence for a function in cell growth.";
 RL Oncogene 8:2607-2615(1993).
 3C -!- FUNCTION: Receptor for thrombopoietin. May represent a regulatory
 3C molecule specific for TPO-R-dependent immune responses.
 3C -!- SUBCELLULAR LOCATION: Type I membrane protein.
 3C -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
 3C Subfamily 1.
 3C -!- SIMILARITY: Contains 2 fibronectin type III domains.
 3C
 3C This SWISS-PROT entry is copyright. It is produced through a collaboration
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 3C use by non-profit institutions as long as its content is in no way
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 3C entities requires a license agreement (See <http://www.isb-eb.ch/announce/>
 3C or send an email to license@isb-eb.ch).
 3C
 3C EMBL; Z22649; CAA80365.1; -;
 3C EMBL; Z22657; CAA80372.1; -;
 3C EMBL; X73677; CAA52031.1; -;
 3C PIR; S35317; S35317.
 3C PIR; S37622; S37622.
 3C HSP; P19235; IERN.
 3C MGD; MGI:197076; Mpl.
 3C InterPro; IPR002996; CRIA.
 3C InterPro; IPR003961; FN III.
 3C InterPro; IPR003528; Hemtopoptn_L_F1.
 3C Pfam; PF00041; fn3; 1.
 3C SMART; SM00060; FN3; 2.
 3C PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
 3C Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
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 3C CHAIN 1 25
 3C DOMAIN 26 625
 3C TRANSMEM 483 504
 3C DOMAIN 505 625
 3C CARBOHYD 117 117
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 3C CONFLICT 99 99
 3C CONFLICT 222 222
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 3C P -> V (IN REF. 2).
 3C P -> PVRTSPAGE (IN REF. 2).
 3C SEQUENCE 625 AA; 69817 MW; 309CF6EAA3724549 CRC64;
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 3C Query Match 11.1%; Score 132.5; DB 1; Length 625;
 3C Best Local Similarity 25.0%; Pred No. 0.0005;
 3C Matches 60; Conservative 25; Mismatches 80; Indels 75; Gaps 14;

QY 4 LVCYTDYLTQVTCILEMWNLPSTLTITWQDYBELKDEATCSLHSAHNAHTATYT-- 61
 DB 281 LQCFTLDLKMVTC-----QWQQ-----DRSSQGFRR--HSRTRCCPTDR 319
 QY 62 -----CHM-----DVHFMAADDIFSVNITDQSGNYSQEGGS- 92
 DB 320 DPTWEKCEEBEPGSGOPALVSRCHFKSRNDSVIHIL-----VEVITTAQGAHVSLGSP 373
 QY 93 FLAESI-KPAPPFNVTTFSGQVNIWSRSDYEDPAPFMLKGLQYLOYNRG-DFWAV 150
 DB 374 FWIHOAVLLPTPSLHWRVSSGRLEWQHOSWAA-----QETCYQLRYTGEGRDMKV 428
 QY 151 -SPRKLISVDSRSVSLPLFRKDSYVELQVRAGPMFGSGSYQGTWSEWSDPVVFQTS 209
 DB 429 LEP-----SLGARGT---LRLPRARYSLQLRA-RLNGPTYQGPWASWPPARVSTGSE 479
 RESULT 15
 LEPR_PIG
 ID LEPR_PIG STANDARD; Q95257; Q9MZS2; Q9N1P9; Q9XSN9;
 AC 002671; Q95257; Q9MZS2; Q9N1P9; Q9XSN9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Leptin receptor precursor (LEP-R) (OB receptor) (OB-R).
 GN LEP-R OR OBR.
 OS Sus scrofa (pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_TaxID=9823;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=20388825; PubMed=10911396;
 RA Ruiz-Cortes Z.T., Men T., Palin M.-F., Downey B.R., Lacroix D.A.,
 RA Murphy B.D.;
 RT "Porcine leptin receptor: molecular structure and expression in the
 RT ovary.";
 RL Mol. Reprod. Dev. 56:465-474(2000).
 RN [2]
 RN SEQUENCE OF 1-123 FROM N.A.
 RC STRAIN=Yorkshire X Meishan.
 RA Lacroix D.A., Gevry N.Y., Ruiz-Cortes Z.T., Murphy B.D.;
 RT "Porcine leptin receptor, intron 3, partial.";
 RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE OF 7-854 FROM N.A.
 RC TISSUE=Liver;
 RA Hu X., Dai R., Li N., Wu C.;
 RT "Expression, detection, and partial cloning of porcine leptin receptor
 RT (OBR) gene.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN SEQUENCE OF 13-159 AND 916-1088 FROM N.A.
 RC TISSUE=Hypothalamus;
 RA Mattern R.L., Carroll J.A.;
 RT "Partial cDNA sequence of the porcine leptin receptor.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RN SEQUENCE OF 109-123 FROM N.A.
 RX MEDLINE=99016721; PubMed=9800339;
 RA Strail A., Kopecky M., Moser G., Schroff J. Jr., Cepica S.;
 RT "HpaII and RsaI PCR-RFLPs within an intron of the porcine leptin
 RT receptor gene (LEPR) and its linkage mapping.";
 RL Anim. Genet. 29:405-406(1998).
 RN [6]
 RN SEQUENCE OF 408-470 FROM N.A.
 RX MEDLINE=97222487; PubMed=9069130;
 RA Ernst C.W., Kapke P.A., Yerle M., Rothschild M.F.;
 RT "The leptin receptor gene (LEPR) maps to porcine chromosome 6.";
 RL Mamm. Genome 8:226-226(1997).
 CC -!- FUNCTION: Receptor for obesity factor (leptin). Involved in the
 CC regulation of fat metabolism and in a hematopoietic pathway

required for normal lymphopoiesis. May play a role in reproduction (By similarity).

!- SUBCELLULAR LOCATION: Type I membrane protein.

!- TISSUE SPECIFICITY: Kidney, liver, spleen, lung, brain, testis, uterus, ovary, corpus luteum, theca and granulosa cells.

!- DOMAIN: The cytoplasmic domain may be essential for intracellular signal transduction by activation of JAK tyrosine kinase and SHRs.

!- PTM: Phosphorylated on two tyrosine residues. Tyr-986 may be the major site of phosphorylation. Phosphorylation on both sites is required for full activity (By similarity).

!- SIMILARITY: Belongs to the type I cytokine family of receptors. Subfamily 2.

!- SIMILARITY: Contains 3 fibronectin type III domains.

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EMBL; AF092422; AAC61766.1; -
 EMBL; AF184173; AAF66822.1; -
 EMBL; AF184172; AAF66822.1; JOINED.
 EMBL; AF16719; AAF89633.1; -
 EMBL; AF036908; AAB88825.1; -
 EMBL; U67739; AAB07892.1; -
 EMBL; AJ223162; CAAL1142.1; -
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 EMBL; U72070; AAC48707.1; -
 HSSP; P16471; 1BP3.
 InterPro; IPR002996; CRIA.
 InterPro; IPR008957; FN III-like.
 InterPro; IPR003961; FN III.
 InterPro; IPR003229; Hemtopoptn_L_F2.
 InterPro; IPR003531; Hemtopoptn_S_F1.
 Pfam; PF00041; FN3; 1.
 SMART; SM00060; FN3; 2.
 PROSITE; PS01353; HEMATOPO REC L F2; 1.
 PROSITE; PS01355; HEMATOPO REC S F1; 1.
 Obesity; Receptor; Transmembrane; Glycoprotein; Signal; Repeat; Phosphorylation.

FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 1165 LEPTIN RECEPTOR.
 FT DOMAIN 22 838 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 839 861 POTENTIAL.
 FT DOMAIN 862 1165 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 237 320 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 537 623 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 738 823 FIBRONECTIN TYPE-III 3.
 FT DISULFID 37 90 BY SIMILARITY.
 FT DISULFID 89 99 BY SIMILARITY.
 FT DISULFID 131 142 BY SIMILARITY.
 FT DISULFID 186 196 BY SIMILARITY.
 FT DISULFID 188 193 BY SIMILARITY.
 FT DISULFID 352 412 BY SIMILARITY.
 FT DISULFID 413 418 BY SIMILARITY.
 FT DISULFID 473 528 BY SIMILARITY.
 FT DISULFID 488 498 BY SIMILARITY.
 FT CARBOHYD 41 41 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 80 80 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).

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 FT CARBOHYD 728 728 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOD_RES 986 986 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 1141 1141 PHOSPHORYLATION (BY SIMILARITY).
 FT CONFLICT 7 9 SVA -> CUV (IN REF. 3).
 FT CONFLICT 69 69 T -> M (IN REF. 3 AND 4).
 FT CONFLICT 73 73 S -> I (IN REF. 1).
 FT CONFLICT 283 283 E -> K (IN REF. 3).
 FT CONFLICT 350 350 F -> L (IN REF. 3).
 FT CONFLICT 362 362 S -> P (IN REF. 3).
 FT CONFLICT 365 365 K -> E (IN REF. 3).
 FT CONFLICT 385 385 G -> S (IN REF. 3).
 FT CONFLICT 974 974 R -> C (IN REF. 4).
 FT CONFLICT 1047 1047 T -> I (IN REF. 4).
 SQ SEQUENCE 1165 AA; 132523 MW; 9F02EADDEDC26D21 CRC64;

Query Match 10.8%; Score 129; DB 1; Length 1165;
 Best Local Similarity 27.2%; Pred. No. 0.0022;
 Matches 47; Conservative 24; Mismatches 56; Indels 46; Gaps 9;

QY 46 CSLHRSAHNATHATYTCM-----DVHFPMADDIFSVNITDSGNYSCGSLFLAE 97
 Db 194 CECHVEV-SAAKLNITLLMYLKITSGAVFTHPLMSVQFINV----- 234
 QY 98 SIKPAPP--FNVTVTFSGQYNISWESDYEDPAFVMLKGLQVLEQYRNGDPWAVSPRK 155
 Db 235 -VKDPPLGLHMEITDGNLKSWSPP-----TLVPQLQVQVKY-SENSTTNMREADE 286
 QY 156 LISVDSRSV-SLLPLEFRKDSSEYELQVRAGMPGSSYOGTWSNSDPVIFQTQ 207
 Db 287 IVSDTSLLVDSVLP-----GSSYEYQVRGKRLDG---PGIWSDNSTPTFTTQ 331

Search completed: March 3, 2004, 12:36:13
 Job time: 9.19281 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 3, 2004, 12:38:15 ; Search time 28.4967 Seconds
(without alignments)
1615.322 Million cell updates/sec

Title: US-09-825-561A-6
Perfect score: 1195
Sequence: 1 CPDLVCYTDYLTQVICILEM.....SDPVFQTSLEKQGNPH 218

Scoring table: BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 809742 seqs, 21115259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1195	100.0	218	9	US-09-825-561A-6
2	1195	100.0	289	9	US-09-941-973-2
3	1195	100.0	538	9	US-09-965-313-2
4	1195	100.0	538	9	US-09-923-246-115
5	1195	100.0	538	9	US-09-825-561A-2
6	1195	100.0	538	10	US-09-972-218A-2
7	1195	100.0	538	14	US-10-264-634-2
8	1195	100.0	538	14	US-10-295-723-115
9	1195	100.0	538	14	US-10-482-622-16
10	1195	100.0	538	14	US-10-243-072-2
11	1195	100.0	538	14	US-10-414-186-2
12	1195	100.0	538	15	US-10-456-780-6
13	1195	100.0	567	9	US-09-825-561A-16
14	1195	100.0	606	9	US-09-923-246-97
15	1195	100.0	606	9	US-09-825-561A-30

16	1195	100.0	606	14	US-10-235-723-97	Sequence 97, Appl
17	1195	100.0	606	14	US-10-243-072-51	Sequence 51, Appl
18	1195	100.0	606	14	US-10-414-186-51	Sequence 51, Appl
19	1188	99.4	538	9	US-09-758-664-2	Sequence 2, Appl
20	1180	98.7	245	14	US-10-264-634-31	Sequence 31, Appl
21	1180	98.7	260	14	US-10-264-634-23	Sequence 23, Appl
22	1180	98.7	467	14	US-10-264-634-25	Sequence 25, Appl
23	1180	98.7	467	14	US-10-264-634-29	Sequence 29, Appl
24	1180	98.7	470	14	US-10-264-634-33	Sequence 33, Appl
25	1180	98.7	492	14	US-10-264-634-27	Sequence 27, Appl
26	1112	93.1	261	9	US-09-825-561A-71	Sequence 71, Appl
27	1077	90.1	247	9	US-09-825-561A-69	Sequence 69, Appl
28	1077	90.1	568	9	US-09-758-664-4	Sequence 4, Appl
29	1077	90.1	568	9	US-09-825-561A-65	Sequence 65, Appl
30	844	70.6	486	9	US-09-825-561A-73	Sequence 73, Appl
31	844	70.6	529	9	US-09-825-561A-12	Sequence 12, Appl
32	844	70.6	529	10	US-09-972-218A-10	Sequence 10, Appl
33	844	70.6	529	14	US-10-264-634-10	Sequence 10, Appl
34	844	70.6	529	14	US-10-243-072-85	Sequence 85, Appl
35	844	70.6	529	14	US-10-414-186-85	Sequence 85, Appl
36	844	70.6	529	15	US-10-418-450-2	Sequence 2, Appl
37	838	70.1	529	9	US-09-965-313-4	Sequence 4, Appl
38	838	70.1	529	9	US-09-732-234-6	Sequence 6, Appl
39	838	70.1	529	9	US-09-784-859-6	Sequence 6, Appl
40	838	70.1	529	13	US-10-076-840-6	Sequence 6, Appl
41	838	70.1	529	15	US-10-624-044-6	Sequence 6, Appl
42	829	69.4	240	14	US-10-264-634-35	Sequence 35, Appl
43	829	69.4	255	14	US-10-264-634-37	Sequence 37, Appl
44	829	69.4	260	14	US-10-264-634-39	Sequence 39, Appl
45	400	33.5	397	14	US-10-243-072-81	Sequence 81, Appl

ALIGNMENTS

RESULT 1
US-09-825-561A-6
; Sequence 6, Application US/09825561A
; Patent No. US20020137677A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. US20020137677A1ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHAL1 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-561A-6

Query Match 100.0%; Score 1195; DB 9; Length 218;
Best Local Similarity 100.0%; Pred. No. 7e-118;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 CPDLVCYTDYLTQVICILEMNLHPSLTITWQOYBELKDEATCSLHRSAAHNTATY 60
QY 61 TCHMDVFFHMADDIFSVNITDQSGNYSCGCSFLAASIKPAPPFNVTVPFGQYNISWR 120
DB 61 TCHMDVFFHMADDIFSVNITDQSGNYSCGCSFLAASIKPAPPFNVTVPFGQYNISWR 120

QY 121 SYEDPAFYMLKGLQYELQYRNRPWAVSPRRKLISVDSRSVSLPLEFRKDSYELQ 180
Db 121 SYEDPAFYMLKGLQYELQYRNRPWAVSPRRKLISVDSRSVSLPLEFRKDSYELQ 180
QY 181 VRAGPMFGSSYQGTWSEWSDPVIFQTSBELKEGWNPH 218
Db 181 VRAGPMFGSSYQGTWSEWSDPVIFQTSBELKEGWNPH 218

RESULT 2

US-09-941-973-2
; Sequence 2, Application US/09941973
; Patent No. US20020160451A1
; APPLICANT: Masiaowski et al.
; TITLE OF INVENTION: NOVEL ORPHAN RECEPTORS
; FILE REFERENCE: REG650
; CURRENT APPLICATION NUMBER: US/09/941,973
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US/09/128,820
; PRIOR FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-941-973-2

Query Match 100.0%; Score 1195; DB 9; Length 289;
Best Local Similarity 100.0%; Pred. No. 1e-117;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TCHMDVFHFMAADDIFSVNITDQSGNYSQCGSFLAESIKPAPPFNVTTFSGQYNISWR 120
Db 80 TCHMDVFHFMAADDIFSVNITDQSGNYSQCGSFLAESIKPAPPFNVTTFSGQYNISWR 139
QY 121 SYEDPAFYMLKGLQYELQYRNRPWAVSPRRKLISVDSRSVSLPLEFRKDSYELQ 180
Db 140 SYEDPAFYMLKGLQYELQYRNRPWAVSPRRKLISVDSRSVSLPLEFRKDSYELQ 199
QY 181 VRAGPMFGSSYQGTWSEWSDPVIFQTSBELKEGWNPH 218
Db 200 VRAGPMFGSSYQGTWSEWSDPVIFQTSBELKEGWNPH 237

RESULT 3

US-09-965-313-2
; Sequence 2, Application US/09965313
; Patent No. US20020090680A1
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; TITLE OF INVENTION: No. US20020090680A1 IL-9/IL-2 Receptor-Like Molecules
; FILE OF INVENTION: and Uses Thereof
; FILE REFERENCE: 5800-17A
; CURRENT APPLICATION NUMBER: US/09/965,313
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/313,913
; PRIOR FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens IL-2/IL-9 Receptor Like
US-09-965-313-2

Query Match 100.0%; Score 1195; DB 9; Length 538;

Best Local Similarity 100.0%; Pred. No. 2.4e-117;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYEEKDEATSCSLHRSAHNATHATY 60
Db 20 CPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYEEKDEATSCSLHRSAHNATHATY 79
QY 61 TCHMDVFHFMAADDIFSVNITDQSGNYSQCGSFLAESIKPAPPFNVTTFSGQYNISWR 120
Db 80 TCHMDVFHFMAADDIFSVNITDQSGNYSQCGSFLAESIKPAPPFNVTTFSGQYNISWR 139
QY 121 SYEDPAFYMLKGLQYELQYRNRPWAVSPRRKLISVDSRSVSLPLEFRKDSYELQ 180
Db 140 SYEDPAFYMLKGLQYELQYRNRPWAVSPRRKLISVDSRSVSLPLEFRKDSYELQ 199
QY 181 VRAGPMFGSSYQGTWSEWSDPVIFQTSBELKEGWNPH 218
Db 200 VRAGPMFGSSYQGTWSEWSDPVIFQTSBELKEGWNPH 237

RESULT 4

US-09-923-246-115
; Sequence 115, Application US/09923246
; Patent No. US20020128446A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020128446Alak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-03-11
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-07-01
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-246-115

Query Match 100.0%; Score 1195; DB 9; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.4e-117;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYEEKDEATSCSLHRSAHNATHATY 60
Db 20 CPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYEEKDEATSCSLHRSAHNATHATY 79
QY 61 TCHMDVFHFMAADDIFSVNITDQSGNYSQCGSFLAESIKPAPPFNVTTFSGQYNISWR 120
Db 80 TCHMDVFHFMAADDIFSVNITDQSGNYSQCGSFLAESIKPAPPFNVTTFSGQYNISWR 139
QY 121 SYEDPAFYMLKGLQYELQYRNRPWAVSPRRKLISVDSRSVSLPLEFRKDSYELQ 180
Db 140 SYEDPAFYMLKGLQYELQYRNRPWAVSPRRKLISVDSRSVSLPLEFRKDSYELQ 199
QY 181 VRAGPMFGSSYQGTWSEWSDPVIFQTSBELKEGWNPH 218
Db 200 VRAGPMFGSSYQGTWSEWSDPVIFQTSBELKEGWNPH 237

RESULT 5

US-09-825-561A-2
; Sequence 2, Application US/09825561A
; Patent No. US20020137677A1

GENERAL INFORMATION:

; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. US20020137677A1ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.

; TITLE OF INVENTION: SOLUBLE ZALPHAL1 CYTOKINE RECEPTORS

; FILE REFERENCE: 00-22

; CURRENT APPLICATION NUMBER: US/09/825.561A

; CURRENT FILING DATE: 2000-04-05

; PRIOR APPLICATION NUMBER: US 60/194,731

; PRIOR FILING DATE: 2000-04-05

; PRIOR APPLICATION NUMBER: US 60/222,121

; PRIOR FILING DATE: 2000-07-28

; NUMBER OF SEQ ID NOS: 86

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 538

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-825-561A-2

Query Match 100.0%; Score 1195; DB 9; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.4e-117;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYBELKDEATSCSLHRSAHNATHATY 60
DB 20 CPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYBELKDEATSCSLHRSAHNATHATY 79
QY 61 TCHMDVHFHMADDDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTTFSGQYNISWR 120
DB 80 TCHMDVHFHMADDDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTTFSGQYNISWR 139
QY 121 SYEDPAPFYMKGKLOYELQYRNRGDPMWVSPRKLISVDSRSVSLLEPLFRKDSSEYELQ 180
DB 140 SYEDPAPFYMKGKLOYELQYRNRGDPMWVSPRKLISVDSRSVSLLEPLFRKDSSEYELQ 199
QY 181 VRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGNPH 218
DB 200 VRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGNPH 237

RESULT 6

US-09-972-218A-2

; Sequence 2, Application US/09972218A
; Publication No. US20030049798A1

GENERAL INFORMATION:

; APPLICANT: Carter, Laura
; APPLICANT: Whitters, Matthew J
; APPLICANT: Collins, Mary
; APPLICANT: Young, Deborah A.
; APPLICANT: Donaldson, Debra D.
; APPLICANT: Lowe, Leslie D.
; APPLICANT: Unger, Michelle

; TITLE OF INVENTION: MU-1, Member of the Cytokine Receptor Family

; FILE REFERENCE: 22058-552CIP2

; CURRENT APPLICATION NUMBER: US/09/972,218A

; CURRENT FILING DATE: 2002-08-19

; PRIOR APPLICATION NUMBER: 09/569384

; PRIOR FILING DATE: 2000-05-11

; PRIOR APPLICATION NUMBER: 09/560766

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US/6057128

; PRIOR FILING DATE: 1998-03-17

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 538

; TYPE: PRT

; ORGANISM: Human

US-09-972-218A-2

Query Match 100.0%; Score 1195; DB 10; Length 538;

Best Local Similarity 100.0%; Pred. No. 2.4e-117;

Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYBELKDEATSCSLHRSAHNATHATY 60
DB 20 CPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYBELKDEATSCSLHRSAHNATHATY 79
QY 61 TCHMDVHFHMADDDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTTFSGQYNISWR 120
DB 80 TCHMDVHFHMADDDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTTFSGQYNISWR 139
QY 121 SYEDPAPFYMKGKLOYELQYRNRGDPMWVSPRKLISVDSRSVSLLEPLFRKDSSEYELQ 180
DB 140 SYEDPAPFYMKGKLOYELQYRNRGDPMWVSPRKLISVDSRSVSLLEPLFRKDSSEYELQ 199
QY 181 VRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGNPH 218
DB 200 VRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGNPH 237

RESULT 7

US-10-264-634-2

; Sequence 2, Application US/10264634

; Publication No. US20030108549A1

GENERAL INFORMATION:

; APPLICANT: Donaldson, Debra et al.

; TITLE OF INVENTION: Methods and Compositions for Modulating Interleukin-21 Receptor A

; FILE REFERENCE: G15320-P3

; CURRENT APPLICATION NUMBER: US/10/264,634

; CURRENT FILING DATE: 2002-10-04

; PRIOR APPLICATION NUMBER: 09/040,005

; PRIOR FILING DATE: 1998-03-17

; PRIOR APPLICATION NUMBER: 09/560,766

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 09/569,384

; PRIOR FILING DATE: 2000-05-11

; PRIOR APPLICATION NUMBER: 09/972,218

; PRIOR FILING DATE: 2001-10-04

; PRIOR APPLICATION NUMBER: 60/373,746

; PRIOR FILING DATE: 2002-04-17

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 538

; TYPE: PRT

; ORGANISM: Human

US-10-264-634-2

Query Match 100.0%; Score 1195; DB 14; Length 538;

Best Local Similarity 100.0%; Pred. No. 2.4e-117;

Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYBELKDEATSCSLHRSAHNATHATY 60
DB 20 CPDLVCYTDYLTQVICILEMNLHPSTLTLTWQDQYBELKDEATSCSLHRSAHNATHATY 79
QY 61 TCHMDVHFHMADDDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTTFSGQYNISWR 120
DB 80 TCHMDVHFHMADDDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTTFSGQYNISWR 139
QY 121 SYEDPAPFYMKGKLOYELQYRNRGDPMWVSPRKLISVDSRSVSLLEPLFRKDSSEYELQ 180
DB 140 SYEDPAPFYMKGKLOYELQYRNRGDPMWVSPRKLISVDSRSVSLLEPLFRKDSSEYELQ 199
QY 181 VRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGNPH 218

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Db 200 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237

RESULT 8
US-10-295-723-115
; Sequence 115, Application US/10295723
; Publication No. US20030125524A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030125524Alak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-723-115

Query Match 100.0%; Score 1195; DB 14; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.4e-117;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVTCILEMWNHLPSTLTWTWQDYELKDEATSCSLHRSAAHATHATY 60
Db 20 CPDLVCYTDYLTQVTCILEMWNHLPSTLTWTWQDYELKDEATSCSLHRSAAHATHATY 79
QY 61 TCHMDVHFHMADDIFSUNITDQSGNYSCGSGFLAESI KPAPPNVTVTFSGQYNISWR 120
Db 80 TCHMDVHFHMADDIFSUNITDQSGNYSCGSGFLAESI KPAPPNVTVTFSGQYNISWR 139
QY 121 SYEDPAFMYLKGKQLQYELQYRNRPDPAVSPRRKLI SVDSRSVSLLLPLEFRKDSYELQ 180
Db 140 SYEDPAFMYLKGKQLQYELQYRNRPDPAVSPRRKLI SVDSRSVSLLLPLEFRKDSYELQ 199
QY 181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
Db 200 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237

RESULT 9
US-10-282-622-16
; Sequence 16, Application US/10282622
; Publication No. US20030134390A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: West, James W.
; APPLICANT: No. US20030134390Alak, Julia E.
; TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/10/282,622
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
; PRIOR FILING DATE: 2001-11-05
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; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-622-16

Query Match 100.0%; Score 1195; DB 14; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.4e-117;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVTCILEMWNHLPSTLTWTWQDYELKDEATSCSLHRSAAHATHATY 60
Db 20 CPDLVCYTDYLTQVTCILEMWNHLPSTLTWTWQDYELKDEATSCSLHRSAAHATHATY 79
QY 61 TCHMDVHFHMADDIFSUNITDQSGNYSCGSGFLAESI KPAPPNVTVTFSGQYNISWR 120
Db 80 TCHMDVHFHMADDIFSUNITDQSGNYSCGSGFLAESI KPAPPNVTVTFSGQYNISWR 139
QY 121 SYEDPAFMYLKGKQLQYELQYRNRPDPAVSPRRKLI SVDSRSVSLLLPLEFRKDSYELQ 180
Db 140 SYEDPAFMYLKGKQLQYELQYRNRPDPAVSPRRKLI SVDSRSVSLLLPLEFRKDSYELQ 199
QY 181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
Db 200 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237

RESULT 10
US-10-243-072-2
; Sequence 2, Application US/10243072
; Publication No. US20030148447A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. US20030148447Alak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZALPHA11
; FILE REFERENCE: 98-55C1
; CURRENT APPLICATION NUMBER: US/10/243,072
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/628,127
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: US 09/404,641
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-243-072-2

Query Match 100.0%; Score 1195; DB 14; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.4e-117;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVTCILEMWNHLPSTLTWTWQDYELKDEATSCSLHRSAAHATHATY 60
Db 20 CPDLVCYTDYLTQVTCILEMWNHLPSTLTWTWQDYELKDEATSCSLHRSAAHATHATY 79
QY 61 TCHMDVHFHMADDIFSUNITDQSGNYSCGSGFLAESI KPAPPNVTVTFSGQYNISWR 120
Db 80 TCHMDVHFHMADDIFSUNITDQSGNYSCGSGFLAESI KPAPPNVTVTFSGQYNISWR 139
QY 121 SYEDPAFMYLKGKQLQYELQYRNRPDPAVSPRRKLI SVDSRSVSLLLPLEFRKDSYELQ 180
```

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Db 140 SYEDPAPYMLKGKQLQYELQYRNKGDPAWSPRKLISVDSRSVSLLPLEFRKDSSEYELQ 199
2y 181 VRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
Db 200 VRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237

RESULT 11
US-10-414-186-2
; Sequence 6, Application US/10414186
; Publication No. US2003017582SA1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. US2003017582SA1ak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHAI1
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/10/414,186
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/09/404,641
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-414-186-2

Query Match 100.0%; Score 1195; DB 14; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.4e-117;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y 1 CPDLVCYTDYLTQVICILEMNNLHPSTLTITWQOYBELKDEATSCSLHRSAHNATHATY 60
2b 20 CPDLVCYTDYLTQVICILEMNNLHPSTLTITWQOYBELKDEATSCSLHRSAHNATHATY 79
2y 61 TCHMDVHFHMADDIFSNITDQSGNYSQECGFLAESIKPAPPFNVTITFSGQYNISWR 120
2b 80 TCHMDVHFHMADDIFSNITDQSGNYSQECGFLAESIKPAPPFNVTITFSGQYNISWR 139
2y 121 SYEDPAPYMLKGKQLQYELQYRNKGDPAWSPRKLISVDSRSVSLLPLEFRKDSSEYELQ 180
2b 140 SYEDPAPYMLKGKQLQYELQYRNKGDPAWSPRKLISVDSRSVSLLPLEFRKDSSEYELQ 199
2y 181 VRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
2b 200 VRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237

RESULT 12
US-10-456-780-6
; Sequence 6, Application US/10456780
; Publication No. US20040009150A1
; GENERAL INFORMATION:
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Hughes, Steven D.
; APPLICANT: Holly, Richard D.
; TITLE OF INVENTION: USE OF IL-21 IN CANCER AND
; FILE REFERENCE: 03-08
; CURRENT APPLICATION NUMBER: US/10/456,780
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/387,127
; PRIOR FILING DATE: 2002-06-07
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; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-456-780-6

Query Match 100.0%; Score 1195; DB 15; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.4e-117;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CPDLVCYTDYLTQVICILEMNNLHPSTLTITWQOYBELKDEATSCSLHRSAHNATHATY 60
Db 20 CPDLVCYTDYLTQVICILEMNNLHPSTLTITWQOYBELKDEATSCSLHRSAHNATHATY 79
Qy 61 TCHMDVHFHMADDIFSNITDQSGNYSQECGFLAESIKPAPPFNVTITFSGQYNISWR 120
Db 80 TCHMDVHFHMADDIFSNITDQSGNYSQECGFLAESIKPAPPFNVTITFSGQYNISWR 139
Qy 121 SYEDPAPYMLKGKQLQYELQYRNKGDPAWSPRKLISVDSRSVSLLPLEFRKDSSEYELQ 180
Db 140 SYEDPAPYMLKGKQLQYELQYRNKGDPAWSPRKLISVDSRSVSLLPLEFRKDSSEYELQ 199
Qy 181 VRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
Db 200 VRAGMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237

RESULT 13
US-09-825-561A-16
; Sequence 16, Application US/09825561A
; Patent No. US20020137677A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. US20020137677Alak, Julia B.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: soluble zalphallr/IgGammal polypeptide
US-09-825-561A-16

Query Match 100.0%; Score 1195; DB 9; Length 567;
Best Local Similarity 100.0%; Pred. No. 2.6e-117;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CPDLVCYTDYLTQVICILEMNNLHPSTLTITWQOYBELKDEATSCSLHRSAHNATHATY 60
Db 20 CPDLVCYTDYLTQVICILEMNNLHPSTLTITWQOYBELKDEATSCSLHRSAHNATHATY 79
Qy 61 TCHMDVHFHMADDIFSNITDQSGNYSQECGFLAESIKPAPPFNVTITFSGQYNISWR 120
Db 80 TCHMDVHFHMADDIFSNITDQSGNYSQECGFLAESIKPAPPFNVTITFSGQYNISWR 139
Qy 121 SYEDPAPYMLKGKQLQYELQYRNKGDPAWSPRKLISVDSRSVSLLPLEFRKDSSEYELQ 180
Db 140 SYEDPAPYMLKGKQLQYELQYRNKGDPAWSPRKLISVDSRSVSLLPLEFRKDSSEYELQ 199
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QY 181 VRAGPMFGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
Db 200 VRAGPMFGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237

RESULT 14

US-09-923-246-97
; Sequence 97, Application US/09923246
; Patent No. US20020128446A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020128446Alak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 97
; LENGTH: 606

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MBP-zalphal1 soluble receptor polypeptide sequence

US-09-923-246-97

Query Match 100.0%; Score 1195; DB 9; Length 606;
Best Local Similarity 100.0%; Pred. No. 2.8e-117;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVICILEMWNLHPSTLTLTWQDQYEEELKDEATCSLHRSAHNATHATY 60
Db 389 CPDLVCYTDYLTQVICILEMWNLHPSTLTLTWQDQYEEELKDEATCSLHRSAHNATHATY 448
QY 61 TCHMDVHFHMADDIFSVNITDQSGNYSCGSGFLLAESIKPAPPFNVTTFSGQYNISWR 120
Db 449 TCHMDVHFHMADDIFSVNITDQSGNYSCGSGFLLAESIKPAPPFNVTTFSGQYNISWR 508
QY 121 SDYEDPAFYMLKGKLOYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSEYELQ 180
Db 509 SDYEDPAFYMLKGKLOYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSEYELQ 568
QY 181 VRAGPMFGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
Db 569 VRAGPMFGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 606

RESULT 15

US-09-825-561A-30
; Sequence 30, Application US/09825561A
; Patent No. US20020137677A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. US20020137677Alak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.

; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MBP-human zalphal1 soluble receptor fusion
; OTHER INFORMATION: polypeptide
; US-09-825-561A-30

Query Match 100.0%; Score 1195; DB 9; Length 606;
Best Local Similarity 100.0%; Pred. No. 2.8e-117;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CPDLVCYTDYLTQVICILEMWNLHPSTLTLTWQDQYEEELKDEATCSLHRSAHNATHATY 60
Db 389 CPDLVCYTDYLTQVICILEMWNLHPSTLTLTWQDQYEEELKDEATCSLHRSAHNATHATY 448
QY 61 TCHMDVHFHMADDIFSVNITDQSGNYSCGSGFLLAESIKPAPPFNVTTFSGQYNISWR 120
Db 449 TCHMDVHFHMADDIFSVNITDQSGNYSCGSGFLLAESIKPAPPFNVTTFSGQYNISWR 508
QY 121 SDYEDPAFYMLKGKLOYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSEYELQ 180
Db 509 SDYEDPAFYMLKGKLOYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSEYELQ 568
QY 181 VRAGPMFGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
Db 569 VRAGPMFGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 606

Search completed: March 3, 2004, 12:50:51
Job time : 28.4967 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 3, 2004, 12:24:04 ; Search time 52.0065 Seconds
(without alignments)
1184.377 Million cell updates/sec

Title: US-09-825-561A-6

Perfect score: 1195

Sequence: 1 CPDLVCVTDYLTQVTCILEM.....SDPVIFQTQSEELKGNPNH 218

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq_29Jan04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1195	100.0	218	5	AAE13728 Human sol
2	1195	100.0	289	3	AAy45029 HUMAN Orp
3	1195	100.0	361	3	AAy69883 Human hae
4	1195	100.0	538	2	AAy27450 Human MU-
5	1195	100.0	538	3	AAb18634 A human z
6	1195	100.0	538	3	AAy45031 HUMAN Orp
7	1195	100.0	538	3	AAy69886 Human hae
8	1195	100.0	538	3	AAy79312 Human cyt
9	1195	100.0	538	4	AAb48001 Human IL-
10	1195	100.0	538	5	ABb81960 Human 164
11	1195	100.0	538	5	AAu11912 Human MU-
12	1195	100.0	538	5	AAe113726 Human sol
13	1195	100.0	538	5	AAu11978 Human zal
14	1195	100.0	538	6	ABR61402 Human IL-
15	1195	100.0	538	6	AAe14939 Human int
16	1195	100.0	538	7	ABu62888 Human MU-
17	1195	100.0	538	7	ABw00881 Human cyt
18	1195	100.0	567	5	AAe13733 Human zal
19	1195	100.0	606	3	AAb18629 Amino aci
20	1195	100.0	606	3	AAy79316 Maltose b
21	1195	100.0	606	5	AAe13736 Maltose b
22	1195	100.0	606	5	AAu11973 MBP-human
23	1195	100.0	606	7	ABw00884 Human Zal
24	1188	99.4	538	3	AAy94304 Human HNO
25	1188	99.4	538	4	AAu08728 Human HNO

26	1187	99.3	471	3	AAy45030	OCR
27	1180	98.7	245	6	ABR61414	Human IL-
28	1180	98.7	260	6	ABR61410	Human IL-
29	1180	98.7	467	6	ABR61413	Human IL-
30	1180	98.7	467	6	ABR61411	Human IL-
31	1180	98.7	470	6	ABR61415	Human IL-
32	1180	98.7	492	6	ABR61412	Human IL-
33	1170	97.9	538	4	AAE02459	Human DNA
34	1159	97.0	538	3	AAy69888	Mouse hae
35	1145	95.8	460	3	AAy69890	Human NR8
36	1138	95.2	375	3	AAy69889	Human NR8
37	1132	93.1	261	5	AAE13742	Human var
38	1077	90.1	247	5	AAE13740	Human SOL
39	1077	90.1	568	3	AAy94305	Human HNO
40	1077	90.1	568	4	AAE02457	Human DNA
41	1077	90.1	568	4	AAU08729	Human HNO
42	1077	90.1	568	5	AAe13738	Human sol
43	844	70.6	486	5	AAE13743	Mouse Zal
44	844	70.6	529	3	AAy79320	Mouse cyt
45	844	70.6	529	5	AAU11915	Mouse MU-

ALIGNMENTS

RESULT 1

AAE13728
ID AAE13728 standard; protein; 218 AA.

XX AC
XX AAE13728;

DT 26-FEB-2002 (first entry)

XX DE Human soluble Zalphall cytokine receptor protein fragment.

XX KW Human; Zalphall; cytokine receptor; immunosuppressive; cytostatic;
KW inflammatory disorder; haemostatic; cell proliferation; immune disorder;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
KW myasthenia gravis; systemic lupus erythematosus; SLE; diabetes; asthma;
KW ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis;
KW viral infection.

XX OS Homo sapiens.

XX PN WO200177171-A2.

XX PD 18-OCT-2001.

XX PF 03-APR-2001; 2001WO-US010872.

XX PR 05-APR-2000; 2000US-0194731P.

XX PR 28-JUL-2000; 2000US-0222121P.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Sprecher CA, Novak JE, West JW, Presnell SR, Holly RD, Nelson AJ;

XX DR WPI; 2002-025898/03.

XX DR N-PSDB; AAD22920.

XX PT Novel soluble receptor polypeptides and polynucleotides used as cytokine
PT antagonist for stimulating ligand activity-induced proliferation of
PT haematopoietic cells and for suppressing immune response in a mammal.

XX PS Claim 27; Page 176-178; 243pp; English.

XX CC The invention relates to an isolated soluble zalphall cytokine receptor
XX polypeptide and their cDNA molecules. Zalpha proteins are useful for
XX inhibiting or antagonising the ligand activity-induced proliferation of
XX haematopoietic cells and haematopoietic cell progenitors preferably
XX lymphoid cells which are natural killer cells or cytotoxic T cells.
XX Zalphall is useful for treating immune and inflammatory disorders, for
XX reducing proliferation of neoplastic B or T cells, for suppressing an

CC immune response in a mammal exposed to an antigen or pathogen. Zalpha is
 CC useful for treating diseases that require immune regulation including
 CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
 CC myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes;
 CC asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease,
 CC sepsis, viral infection (dengue virus infection) and cancer. The present
 CC sequence is human soluble Zalpha cytokine receptor protein fragment
 XX
 SQ Sequence 218 AA;

Query Match 100.0%; Score 1195; DB 5; Length 218;
 Best Local Similarity 100.0%; Pred. No. 4.3e-115;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLVQVICILEMNLHPSTLTITWQDQYEELKDEATCSLHRSAHNATHATY 60
 DB 1 CPDLVCYTDYLVQVICILEMNLHPSTLTITWQDQYEELKDEATCSLHRSAHNATHATY 60
 QY 61 TCHMDVHFHFWADDFISVNTDQSGNYSQCGSFLLAESIKPAPPFNVTTFSGQYNISWR 120
 DB 61 TCHMDVHFHFWADDFISVNTDQSGNYSQCGSFLLAESIKPAPPFNVTTFSGQYNISWR 120
 QY 121 SYEDPAFYMLKGLQYELQYRNRPDPWAVSPRKLISVDSRSVSLLPLEFRKDSSEYELQ 180
 DB 121 SYEDPAFYMLKGLQYELQYRNRPDPWAVSPRKLISVDSRSVSLLPLEFRKDSSEYELQ 180
 QY 181 VRAGPMGSSYQGTWSEWSDPVIFQTSBELKEGWNPH 218
 DB 181 VRAGPMGSSYQGTWSEWSDPVIFQTSBELKEGWNPH 218

RESULT 2
 AAY45029
 ID AAY45029 standard; protein; 289 AA.

XX AAY45029;

XX 31-MAY-2000 (first entry)

XX HUMAN Orphan Cytokine Receptor-10 (OCR10) polypeptide.

XX Human; Orphan Cytokine Receptor-10; OCR10; chromosome 16p12; cytokine;
 XX screen; cognate ligand; treatment; endocrine disorder; immune disorder.

XX Homo sapiens.

XX Key Location/Qualifiers
 XX Peptide 4..21
 XX /label= Signal_peptide
 XX Protein 22..289
 XX /label= Mature_HUMAN_OCR10
 XX Region 118..169
 XX /label= Proline_hinge_motif_region
 XX Domain 122..123
 XX /label= Proline_hinge_motif
 XX Domain 238..255
 XX /label= Transmembrane_domain
 XX /note= "Putative and hydrophobic"
 XX Region 263..278
 XX /label= Jak-binding_region
 XX /note= "Potential"

XX W0200008152-A1.

XX 17-FEB-2000.

XX 16-JUL-1999; 99WO-US016060.

XX 04-AUG-1998; 98US-00128820.

XX (REGE-) REGENERON PHARM INC.

XX Masiakowski PJ, Morris J, Valenzuela DM;

XX WPI; 2000-205707/18.
 DR N-PSDB; AAZ50746.
 XX New HUMAN orphan cytokine receptors 10 and 10-A useful for screening for
 PT drugs e.g. receptor agonists that may mediate survival and
 PT differentiation in cells naturally expressing the receptor and for
 PT screening for cognate ligands.

XX Example 1; Page 21; 54pp; English.

XX The present sequence is the HUMAN Orphan Cytokine Receptor-10 (OCR10)
 CC polypeptide. HUMAN OCR10 gene is located on chromosome 16p12. It is
 CC expressed at high levels in spleen, thymus, peripheral blood leucocytes
 CC and lymph nodes and moderately in heart and placenta. It has a role in
 CC immune system and cytokine function. It is useful in screening for
 CC cognate ligands or drugs that mediate survival and differentiation of
 CC cells expressing this receptor. Modified HUMAN OCR10 or its agonist can
 CC be used in the treatment of endocrine or immune disorders

XX Sequence 289 AA;

Query Match 100.0%; Score 1195; DB 3; Length 289;

Best Local Similarity 100.0%; Pred. No. 6.4e-115;

Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLVQVICILEMNLHPSTLTITWQDQYEELKDEATCSLHRSAHNATHATY 60
 DB 20 CPDLVCYTDYLVQVICILEMNLHPSTLTITWQDQYEELKDEATCSLHRSAHNATHATY 79
 QY 61 TCHMDVHFHFWADDFISVNTDQSGNYSQCGSFLLAESIKPAPPFNVTTFSGQYNISWR 120
 DB 80 TCHMDVHFHFWADDFISVNTDQSGNYSQCGSFLLAESIKPAPPFNVTTFSGQYNISWR 139
 QY 121 SYEDPAFYMLKGLQYELQYRNRPDPWAVSPRKLISVDSRSVSLLPLEFRKDSSEYELQ 180
 DB 140 SYEDPAFYMLKGLQYELQYRNRPDPWAVSPRKLISVDSRSVSLLPLEFRKDSSEYELQ 199
 QY 181 VRAGPMGSSYQGTWSEWSDPVIFQTSBELKEGWNPH 218
 DB 200 VRAGPMGSSYQGTWSEWSDPVIFQTSBELKEGWNPH 237

RESULT 3

AAY69883

ID AAY69883 standard; protein; 361 AA.

XX AAY69883;

XX 24-MAY-2000 (first entry)

XX Human haemopoietin receptor family member NR8alpha.

XX Haemopoietin receptor family; NR8; antibody; diagnosis;
 XX blood formation disorder.

XX Homo sapiens.

XX W09967290-A1.

XX 29-DEC-1999.

XX 23-JUN-1999; 99WO-JP003351.

XX 24-JUN-1998; 98JP-00214720.

XX 19-OCT-1998; 98JP-00297409.

XX (CHUS) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX Nomura H, Maeda M;

XX WPI; 2000-116933/10.

XX N-PSDB; AAZ59237.

XX Hemopoietin receptor protein family NR8 used for diagnosis of blood
 PT formation disorders.
 XX
 XX Claim 1; Fig 5-6; 176pp; Japanese.
 XX
 XX This sequence represents a novel haemopoietin receptor protein family
 CC NR8, designated NR8alpha. Antibodies to the NR8 family proteins are used
 CC for the diagnosis of blood formation disorders. Compounds identified as
 CC binding to the proteins are used for the treatment of such disorders
 XX
 XX Sequence 361 AA;

Query Match 100.0%; Score 1195; DB 3; Length 361;
 Best Local Similarity 100.0%; Pred. No. 8.9e-115; Indels 0; Gaps 0;
 Matches 218; Conservative 0; Mismatches 0;

QY 1 CPDLVCTDYLTQVTCILEMNLHPSLTTLTWQDYELKDEATCSLHRSANATHATY 60
 DB 20 CPDLVCTDYLTQVTCILEMNLHPSLTTLTWQDYELKDEATCSLHRSANATHATY 79
 QY 61 TCHMDVHFHMADDDIFSVNITDQSGNYSQECGFLLAESIKPAPPFNVTVPFGQYNISWR 120
 DB 80 TCHMDVHFHMADDDIFSVNITDQSGNYSQECGFLLAESIKPAPPFNVTVPFGQYNISWR 139
 QY 121 SDYEDPAFVMLKGKLYELOYENRGDPWAVSPRKLISVDSRSVSLLPLEFRKDSYELQ 180
 DB 140 SDYEDPAFVMLKGKLYELOYENRGDPWAVSPRKLISVDSRSVSLLPLEFRKDSYELQ 199
 QY 181 VRAGPMPGSSYQGTWSESDPVIQTQSEELKEGNPH 218
 DB 200 VRAGPMPGSSYQGTWSESDPVIQTQSEELKEGNPH 237

RESULT 4
 AAY27450
 ID AAY27450 standard; protein; 538 AA.
 XX
 XX AAY27450;
 AC
 DT 26-NOV-1999 (first entry)
 XX
 XX Human MU-1 hematopoietin receptor protein.

XX MU-1 hematopoietin receptor protein; e MU-1 protein; gene therapy;
 KW cell proliferation; cytokine production; immune response; cancer;
 KW autoimmune disease; transplant rejection; hematopoiesis; anemia;
 KW gene mapping; nutritional supplement; human.

XX Homo sapiens.
 XX WO9947675-A1.
 XX
 XX 23-SEP-1999.
 XX
 XX 17-MAR-1999; 99WO-US005854.
 XX
 XX 17-MAR-1998; 98US-00040005.
 XX
 XX (GEMY) GENETICS INST INC.
 XX
 XX Donaldson D, Ungar M;
 XX
 XX WPI: 1999-562115/47.
 XX
 XX N-PSDB; AA207535.

XX New nucleic acid encoding the MU-1 hematopoietin receptor protein, used
 PT for treating e.g. cancer, autoimmune disease or abnormal hematopoiesis.
 XX
 XX Claim 9; Page 33-35; 37pp; English.

XX This represents a MU-1 hematopoietin receptor protein. The protein can be
 CC produced by standard recombinant methodology. The MU-1 protein has the

CC biological activity of the MU-1 hematopoietin receptor superfamily chain.
 IT, is used to screen for specific binding agents; to raise specific
 CC antibodies; as assay reagents, tissue markers etc. and therapeutically
 CC (optionally expressed from the MU-1 gene by gene therapy). Many possible
 CC activities/uses of the MU-1 protein are described without supporting
 CC evidence, e.g. they regulate cell proliferation and differentiation,
 CC induce production of cytokines, stimulate or suppress an immune response
 CC (e.g. for treating immune deficiency of any etiology, cancer or
 CC autoimmune disease, and for preventing transplant rejection) and regulate
 CC of hematopoiesis, e.g. for treating anemia. The MU-1 gene is used as a
 CC research reagent, for recombinant production of the protein, as tissue or
 CC molecular weight marker, for gene mapping; for production of anti-DNA or
 CC anti-protein antibodies etc. The MU-1 protein and the nucleic acids are
 CC also useful as nutritional supplements or sources and the antibodies can
 CC be used therapeutically, as assay reagents and for affinity purification
 XX
 XX Sequence 538 AA;

Query Match 100.0%; Score 1195; DB 2; Length 538;
 Best Local Similarity 100.0%; Pred. No. 1.6e-114;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCTDYLTQVTCILEMNLHPSLTTLTWQDYELKDEATCSLHRSANATHATY 60
 DB 20 CPDLVCTDYLTQVTCILEMNLHPSLTTLTWQDYELKDEATCSLHRSANATHATY 79
 QY 61 TCHMDVHFHMADDDIFSVNITDQSGNYSQECGFLLAESIKPAPPFNVTVPFGQYNISWR 120
 DB 80 TCHMDVHFHMADDDIFSVNITDQSGNYSQECGFLLAESIKPAPPFNVTVPFGQYNISWR 139
 QY 121 SDYEDPAFVMLKGKLYELOYENRGDPWAVSPRKLISVDSRSVSLLPLEFRKDSYELQ 180
 DB 140 SDYEDPAFVMLKGKLYELOYENRGDPWAVSPRKLISVDSRSVSLLPLEFRKDSYELQ 199
 QY 181 VRAGPMPGSSYQGTWSESDPVIQTQSEELKEGNPH 218
 DB 200 VRAGPMPGSSYQGTWSESDPVIQTQSEELKEGNPH 237

RESULT 5
 AAB18634
 ID AAB18634 standard; protein; 538 AA.
 XX
 XX AAB18634;
 AC
 DT 22-JAN-2001 (first entry)
 XX
 XX A human zalphall ligand polypeptide.
 XX
 XX zalphall ligand; cytokine; haematopoietic cell proliferation; lymphoma;
 KW tumorigenesis; leukaemia; hematopoiesis; B cell tumour.

XX Homo sapiens.

XX WO2000053761-A2.

XX 14-SEP-2000.

XX 09-MAR-2000; 2000WO-US006067.

XX 09-MAR-1999; 99US-00264908.

XX 11-MAR-1999; 99US-00265992.

XX 01-JUL-1999; 99US-0142013P.

XX (ZYMO) ZYMOGENETICS INC.

XX Novak JB, Presnell SR, Sprecher CA, Foster DC, Holly RD;

PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;

XX WPI: 2000-565600/52.

XX N-PSDB; AAA75557.

XX New human cytokine, designated zalphall ligand, useful for stimulating

PT the proliferation and/or development of hematopoietic cells in vitro and
 PT in vivo, and for treating tumorigenesis.

PS Disclosure; Page 255-256; 256pp; English.

XX The present sequence represents a human zalphall ligand polypeptide,
 CC which is a cytokine. The zalphall ligand is useful for stimulating the
 CC proliferation and development of hematopoietic cells in vitro and in
 CC vivo. Zalphall ligand polynucleotides can be used as primers or probes
 CC for cloning the zalphall gene. The zalphall ligand is useful for treating
 CC tumorigenesis. A zalphall ligand-saporin fusion toxin may be used for
 CC treating leukaemias and lymphomas. Antagonists against zalphall ligand
 CC are useful as research reagents for characterizing ligand-receptor
 CC interaction. Antagonists are also useful for inhibiting expansion,
 CC proliferation, activation and differentiation of cells involved in
 CC regulating hematopoiesis. The zalphall ligand may also be used to
 CC stimulate an immune response against B cell tumour, a virus, a parasite
 CC or a bacterium. The zalphall polypeptides, polynucleotides, antagonists,
 CC agonists and antibodies are also useful for the detection, diagnosis,
 CC prevention, and treatment of diseases associated with a zalphall ligand
 CC genetic defect

XX Sequence 538 AA;

Query Match 100.0%; Score 1195; DB 3; Length 538;
 Best Local Similarity 100.0%; Pred. No. 1.6e-114;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVICILEMNLHPSTLTITWQDQYEELKDEATSCSLHRSAHNATHATY 60
 DB 20 CPDLVCYTDYLTQVICILEMNLHPSTLTITWQDQYEELKDEATSCSLHRSAHNATHATY 79
 QY 61 TCHMDVFHFMAADDIFSVNITDQSGNYSQCGSFLLAESIKPAPPFNVTTFSGQYNISWR 120
 DB 80 TCHMDVFHFMAADDIFSVNITDQSGNYSQCGSFLLAESIKPAPPFNVTTFSGQYNISWR 139
 QY 121 SDYEDPAFYMLKGLQYELQYRNRPDPWAVSPRKLISVDSRSVLLPLEFRKDSYELQ 180
 DB 140 SDYEDPAFYMLKGLQYELQYRNRPDPWAVSPRKLISVDSRSVLLPLEFRKDSYELQ 199
 QY 181 VRAGPMFGSSYQGTWSESDPVIQTQSEBELKEGWNPH 218
 DB 200 VRAGPMFGSSYQGTWSESDPVIQTQSEBELKEGWNPH 237

RESULT 6

AA45031
 ID AAY45031 standard; protein; 538 AA.

XX AAY45031;
 XX AC
 XX DT 31-MAY-2000 (first entry)
 XX DE HUMAN Orphan Cytokine Receptor 10 (OCR10)-A polypeptide.

XX Human; Orphan Cytokine Receptor 10-A; OCR10-A; cytokine; screen;
 XX cognate ligand; treatment; endocrine disorder; immune disorder.

XX Homo sapiens.

XX WO200008152-A1.

XX 17-FEB-2000.

XX 16-JUL-1999; 99WO-US016060.

XX 04-AUG-1998; 98US-00128820.

XX (REGE-) REGENERON PHARM INC.

XX Masiakowski PJ, Morris J, Valenzuela DM;

XX WPI; 2000-205707/18.

DR N-PSDB; AAZ50749.

XX New HUMAN orphan cytokine receptors 10 and 10-A useful for screening for
 PT drugs e.g. receptor agonists that may mediate survival and
 PT differentiation in cells naturally expressing the receptor and for
 PT screening for cognate ligands.

XX Example 10; Page 39-41; 54pp; English.

XX The present sequence is that of HUMAN Orphan Cytokine Receptor 10-A
 CC (OCR10-A) polypeptide. It is expressed at high levels in spleen, thymus,
 CC peripheral blood leucocytes and lymph nodes and moderately in heart and
 CC placenta. It has a role in immune system and cytokine function. It is
 CC useful in screening for cognate ligands or drugs that mediate survival
 CC and differentiation of cells expressing this receptor. Modified HUMAN
 CC OCR10-A or its agonist can be used in the treatment of endocrine or
 CC immune disorders

XX Sequence 538 AA;

Query Match 100.0%; Score 1195; DB 3; Length 538;
 Best Local Similarity 100.0%; Pred. No. 1.6e-114;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVICILEMNLHPSTLTITWQDQYEELKDEATSCSLHRSAHNATHATY 60
 DB 20 CPDLVCYTDYLTQVICILEMNLHPSTLTITWQDQYEELKDEATSCSLHRSAHNATHATY 79
 QY 61 TCHMDVFHFMAADDIFSVNITDQSGNYSQCGSFLLAESIKPAPPFNVTTFSGQYNISWR 120
 DB 80 TCHMDVFHFMAADDIFSVNITDQSGNYSQCGSFLLAESIKPAPPFNVTTFSGQYNISWR 139
 QY 121 SDYEDPAFYMLKGLQYELQYRNRPDPWAVSPRKLISVDSRSVLLPLEFRKDSYELQ 180
 DB 140 SDYEDPAFYMLKGLQYELQYRNRPDPWAVSPRKLISVDSRSVLLPLEFRKDSYELQ 199
 QY 181 VRAGPMFGSSYQGTWSESDPVIQTQSEBELKEGWNPH 218
 DB 200 VRAGPMFGSSYQGTWSESDPVIQTQSEBELKEGWNPH 237

RESULT 7

AA45986

ID AAY69886 standard; protein; 538 AA.

XX AAY69886;

XX AC

XX DT 24-MAY-2000 (first entry)

XX Human haemopoietin receptor family member NR8gamma.

XX Haemopoietin receptor family; NR8; antibody; diagnosis;

XX blood formation disorder.

XX Homo sapiens.

XX WO9967290-A1.

XX 29-DEC-1999.

XX 23-JUN-1999; 99WO-JP003351.

XX 24-JUN-1998; 98JP-00214720.

XX 19-OCT-1998; 98JP-00297409.

XX (CHUS) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX Nomura H, Maeda M;

XX WPI; 2000-116933/10.

XX N-PSDB; AAZ59240.

XX Hemopoietin receptor protein family NR8 used for diagnosis of blood

PT formation disorders.
PS Claim 4; Fig 9-10; 176pp; Japanese.
XX This sequence represents a novel haemolectin receptor protein family
XX NR8, designated NR8gamma. Antibodies to the NR8 family proteins are used
CC for the diagnosis of blood formation disorders. Compounds identified as
CC binding to the proteins are used for the treatment of such disorders
XX
SQ Sequence 538 AA;

Query Match 100.0%; Score 1195; DB 3; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.6e-114;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVTCILEMNLHPSTLTWQDQYELKDEATSCSLHRSAAHATHATY 60
DB 20 CPDLVCYTDYLTQVTCILEMNLHPSTLTWQDQYELKDEATSCSLHRSAAHATHATY 79
QY 61 TCHMDVHFHMADDFSVNITDQSGNYSCGSLFLAESIKPAPPFNVTVTFSGQYNISWR 120
DB 80 TCHMDVHFHMADDFSVNITDQSGNYSCGSLFLAESIKPAPPFNVTVTFSGQYNISWR 139
QY 121 SDYEDPAFYMKGKQLQYELQYRNRGDPWAVSPRKLISVDSRSVSLLPLEFRKDSYELQ 180
DB 140 SDYEDPAFYMKGKQLQYELQYRNRGDPWAVSPRKLISVDSRSVSLLPLEFRKDSYELQ 199
QY 181 VRAGPMGSSVQGTWSESDPVIPTQSEELKEGWNPH 218
DB 200 VRAGPMGSSVQGTWSESDPVIPTQSEELKEGWNPH 237

RESULT 8
ID AAY79312
XX AAY79312 standard; protein; 538 AA.
AC AAY79312;
XX
DT 18-JUL-2000 (first entry)
XX
DE Human cytokine receptor zalphall.
XX
KW Cytokine receptor; zalphall; human; chromosome 16p11.1; apoptosis;
KW signal transduction; growth factor; cancer; tumour; infection;
KW immunosuppressive; immunostimulant; autoimmune disease; leukaemia;
KW lymphoma; transplant rejection; therapy; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 1..19
FT Peptide /note= "signal peptide"
FT Protein 20..538
FT /note= "mature protein; a polypeptide comprising the
FT mature protein is specifically claimed in Claim 27(d)"
FT Domain 20..237
FT /note= "cytokine-binding domain; a polypeptide comprising
FT this domain is specifically claimed in Claim 27(a)"
FT Domain 192..202
FT /note= "penultimate strand region"
FT Region 214..218
FT /note= "WSXWS motif"
FT Domain 238..255
FT /note= "transmembrane domain"
FT Domain 256..538
FT /note= "intracellular signalling domain; a polypeptide
FT comprising this domain is specifically claimed in Claim
FT 27(c)"
FT Region 267..273
FT /note= "Box I signalling site"
FT Region 301..304
FT /note= "Box II signalling site"
XX

PN WO200017235-A2.
XX
PD 30-MAR-2000.
XX
XX 23-SEP-1999; 99WO-US022149.
XX
XX 23-SEP-1998; 98US-00159254.
PR 09-MAR-1999; 99US-00285117.
PR 06-JUL-1999; 99US-00347930.
XX
XX (ZYMO) ZYMOGENETICS INC.
PA
PI Presnell SR, Conklin DC, Novak JE, Hammond AK;
XX
XX WPI: 2000-292825/25.
DR N-PSDB; AA294533, AA294534.
XX
XX Novel nucleic acid encoding zalphall polypeptide, useful for treating
PT e.g. viral infection or tumors, and for identifying ligands that
PT stimulate cell proliferation.
XX
PS Claim 27(e); Page 148-149; 190pp; English.
XX
XX The present sequence is that of zalphall, a novel human class I cytokine
CC receptor that may be involved in an apoptotic cellular pathway, or is a
CC cell signalling molecule, growth factor receptor, or extracellular
CC matrix associated protein with growth factor hormone activity. The
CC sequence was deduced from a cDNA clone (see AA294533) isolated from a
CC spinal cord library. Polypeptides comprising amino acids 20-237, 20-255,
CC 256-538, 20-538 and 1-538 of the present sequence are claimed. Zalphall
CC is expressed in lymph node, peripheral blood leucocytes, spleen and
CC thymus. The mRNA is also abundant in the Raji cell line (ATCC CCL 86)
CC derived from Burkitt's lymphoma. Zalphall polypeptides, and fusion
CC proteins including them, can be obtained by expression in recombinant
CC host cells. They are used: to detect ligands (also ligand agonists and
CC antagonists) that stimulate proliferation and/or development of
CC haematopoietic, lymphoid and myeloid cells, in vitro or in vivo, e.g. as
CC a replacement for serum in culture media; in soluble form to block ligand
CC activity (direct antagonists) and to detect ligand-expressing cancers; to
CC raise specific antibodies; and for purification of cognate ligands.
CC Agonistic ligands may stimulate cell-mediated immunity, e.g. for treating
CC (viral) infections associated with immunosuppression, improving the
CC activity of vaccines, suppressing tumours, treating leukaemia and
CC improving T-cell regeneration after bone marrow transplant. Antagonists
CC are useful as immunosuppressants, e.g. in the treatment of autoimmune
CC disease (e.g. rheumatoid arthritis, multiple sclerosis, diabetes), to
CC prevent transplant rejection and to treat T-cell leukemia or lymphoma
XX
XX Sequence 538 AA;
SQ

Query Match 100.0%; Score 1195; DB 3; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.6e-114;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVTCILEMNLHPSTLTWQDQYELKDEATSCSLHRSAAHATHATY 60
DB 20 CPDLVCYTDYLTQVTCILEMNLHPSTLTWQDQYELKDEATSCSLHRSAAHATHATY 79
QY 61 TCHMDVHFHMADDFSVNITDQSGNYSCGSLFLAESIKPAPPFNVTVTFSGQYNISWR 120
DB 80 TCHMDVHFHMADDFSVNITDQSGNYSCGSLFLAESIKPAPPFNVTVTFSGQYNISWR 139
QY 121 SDYEDPAFYMKGKQLQYELQYRNRGDPWAVSPRKLISVDSRSVSLLPLEFRKDSYELQ 180
DB 140 SDYEDPAFYMKGKQLQYELQYRNRGDPWAVSPRKLISVDSRSVSLLPLEFRKDSYELQ 199
QY 181 VRAGPMGSSVQGTWSESDPVIPTQSEELKEGWNPH 218
DB 200 VRAGPMGSSVQGTWSESDPVIPTQSEELKEGWNPH 237

RESULT 9
AAB48001

ID AAB48001 standard; protein; 538 AA.
 AC AAB48001;
 XX
 XX 19-MAR-2001 (first entry)
 XX
 XX Human IL-9/IL-2 receptor-like 16445 protein.
 XX
 XX Interleukin-9; IL-9; IL-2 receptor; 16445 protein; inflammatory;
 KW I-lymphocyte-related disorder; antithyroid; antiproliferative; human;
 KW immunosuppressive; antidiabetic; antidiabetic; antidiabetic; antidiabetic;
 KW antidiabetic; nephrotropic; gene therapy.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 PH Peptide 1..19
 FT /note= "signal peptide"
 FT Protein 20..538
 FT /note= "mature protein"
 XX
 XX W0200069880-A1.
 XX
 XX 23-NOV-2000.
 XX
 XX 18-MAY-2000; 2000WO-US013687.
 XX
 XX 18-MAY-1999; 99US-00313913.
 XX
 XX (MILL-) MILLENNIUM PHARM INC.
 XX
 XX Hodge MR;
 XX
 XX WPI; 2001-016209/02.
 DR N-PSDB; AAC84147.
 DR
 XX Novel interleukin-9/interleukin-2 receptor-like polypeptides useful for
 PT diagnosis and treatment immune, inflammatory and respiratory disorders
 PT and in screening assays for identifying modulators.
 XX
 XX Claim 8; Page 104-106; 119pp; English.
 XX
 XX The invention relates to isolated human and murine interleukin-9 (IL-9)
 CC /IL-2 receptor-like polypeptides. The plasmid containing the encoding
 CC cDNA insert is deposited as ATCC PTA-350. The IL-9/IL-2 receptor-like
 CC polypeptides (16445 proteins) can be recombinantly produced using
 CC standard recombinant methodology. The 16445 proteins are used for
 CC identifying their modulators and for diagnosis and treatment of immune,
 CC inflammatory and respiratory disorders and disorders associated with
 CC lungs, colon, kidney and lymphoid tissues including tonsil and thymus, in
 CC particular T-lymphocyte-related disorders including atopic conditions
 CC such as asthma, allergy, rheumatoid arthritis, psoriasis, chronic
 CC inflammatory diseases and graft versus host disease, disorders involving
 CC the colon such as diarrhoea, dysentery, infectious enterocolitis, kidney
 CC disorders including polyostic kidney disease, cystic renal dysplasia,
 CC disorders of the thymus including lymphomas, Hodgkin disease and
 CC carcinoids. The 16445 polypeptides are also useful as modulating agents
 CC in cellular processes including growth promoting activity, particularly
 CC the antigen-independent proliferation of T-helper cell clones. The
 CC encoding nucleic acid is useful as primers or hybridization probes for
 CC the detection of IL-9/IL-2 receptor-like encoding nucleic acids and for
 CC tissue typing and in forensic biology. The present sequence represents
 CC the human IL-9/IL-2 receptor-like polypeptide (AAH16445)
 XX
 XX Sequence 538 AA;
 SQ
 Query Match 100.0%; Score 1195; DB 4; Length 538;
 Best Local Similarity 100.0%; Pred. No. 1.6e-114; Indels 0; Gaps 0;
 Matches 216; Conservative 0; Mismatches 0;
 QY 1 CPDLVCYTDYQVIGILEMNLHPSTLTITWQDQVEELKDEATSCSLRSAAHATHATY 60
 DB 20 CPDLVCYTDYQVIGILEMNLHPSTLTITWQDQVEELKDEATSCSLRSAAHATHATY 79

QY 61 TCHMDVHFHADDIFSVNITDQGNYSQBCGSFLAESIKPAPPFNVTTFSCQYNISWR 120
 DB 80 TCHMDVHFHADDIFSVNITDQGNYSQBCGSFLAESIKPAPPFNVTTFSCQYNISWR 139
 QY 121 SDYEDPAFYMLKGLQYELQYRNKGDPAVSPRKLISVDNRSLVLLPLEFRKDSYELQ 180
 DB 140 SDYEDPAFYMLKGLQYELQYRNKGDPAVSPRKLISVDNRSLVLLPLEFRKDSYELQ 199
 QY 181 VRAGMPGSSVQGTWSEWSDPVIFQTOSELKKGWNP 218
 DB 200 VRAGMPGSSVQGTWSEWSDPVIFQTOSELKKGWNP 237

RESULT 10
 ABB81960
 ID ABB81960 standard; protein; 538 AA.
 XX
 AC ABB81960;
 XX
 XX 25-NOV-2002 (first entry)
 XX
 XX Human 16445 protein.
 XX
 XX Interleukin; IL-9; IL-2; 16445; antidiabetic; antidiabetic; human;
 KW antiproliferative; antidiabetic; immunosuppressive; cytostatic; virucide;
 KW antirheumatic; antidiabetic; antidiabetic; antidiabetic; dermatological;
 KW nephrotropic; antidiabetic; tuberculostatic; antileptotic; antipyloric;
 KW antileptic; gene therapy; receptor.
 XX
 OS Homo sapiens.
 XX
 XX US2002090680-A1.
 XX
 XX 11-JUL-2002.
 XX
 XX 26-SEP-2001; 2001US-00965313.
 XX
 XX 18-MAY-1999; 99US-00313913.
 XX
 XX 18-MAY-2000; 2000US-00574100.
 XX
 XX (MILL-) MILLENNIUM PHARM INC.
 XX
 XX Hodge MR;
 XX
 XX WPI; 2002-655832/70.
 DR N-PSDB; ABQ79536.
 XX
 XX New interleukin-9/interleukin-2 receptor-like polypeptides and
 PT polynucleotides for diagnosing, treating respiratory, T-lymphocyte
 PT related disorders and disorders associated with lung, colon, kidney and
 PT lymphoid tissues.
 XX
 XX Claim 8; Page 31-33; 54pp; English.
 XX
 XX The invention relates to isolated interleukin (IL)-9/IL-2 receptor-like
 CC polypeptide, 16445. The 16445 polypeptides can be expressed by standard
 CC recombinant methodology. The 16445 polypeptide, polynucleotides and their
 CC modulators are useful for modulating the immune, inflammatory and
 CC respiratory responses, for the diagnosis and treatment of immune and
 CC respiratory disorders, particularly for the treatment and diagnosis of T-
 CC lymphocyte-related disorders, including, atopic conditions, such as
 CC asthma and allergy, including allergic rhinitis, psoriasis, the effects
 CC of pathogen infection, chronic inflammatory diseases, organ-specific
 CC autoimmunity, graft rejection, and graft versus host disease. The
 CC molecules are also useful as modulating agents in a variety of cellular
 CC processes including growth promoting activity, particularly the antigen
 CC independent proliferation of T-helper cell clones, and direct effects on
 CC normal haemopoietic progenitors, human T cells, B cells, thymocytes,
 CC thymic lymphomas and neuronal cell lines. They are useful for the
 CC modulation, diagnosis, and treatment of immune, inflammatory, and
 CC respiratory disorders and disorders associated with lungs, colon, kidney,
 CC and lymphoid tissues including tonsil and thymus. The present sequence

CC represents a human 16445 polypeptide

XX Sequence 538 AA;

Query Match 100.0%; Score 1195; DB 5; Length 538;
 Best Local Similarity 100.0%; Pred. No. 1.6e-114;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY 60
 DB 20 CPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY 79
 QY 61 TCHMDVHFHMADDFISVNTDQSGNSQCGSFLLAESIKPAPPFNVTTFSGQYNISWR 120
 DB 80 TCHMDVHFHMADDFISVNTDQSGNSQCGSFLLAESIKPAPPFNVTTFSGQYNISWR 139
 QY 121 SYDEDPAFYMLKGLQYELQYRNRGDPWAVSPRKLISVDSRSVSLPLEFRKDSSEYELQ 180
 DB 140 SYDEDPAFYMLKGLQYELQYRNRGDPWAVSPRKLISVDSRSVSLPLEFRKDSSEYELQ 199
 QY 181 VRAGPMGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
 DB 200 VRAGPMGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237

RESULT 11

AD AAU11912 standard; protein; 538 AA.

XX AAU11912;

XX 09-APR-2002 (first entry)

XX Human MU-1 haematopoietin receptor superfamily chain protein sequence.

XX Human; MU-1; haematopoietin receptor superfamily chain; thyroiditis;
 KW immune deficiency; anaemia; autoimmune disorder; multiple sclerosis;
 KW systemic lupus erythematosus; rheumatoid arthritis;
 KW pulmonary inflammation; insulin dependent diabetes mellitus;
 KW nutritional supplement; cytokine receptor family.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Domain 237..254
 FT /note= "Transmembrane domain"

XX WO200185792-A2.

XX 15-NOV-2001.

XX 11-MAY-2001; 2001WO-US015395.

XX 05-NOV-1999; 99US-00569384.

XX (GENY) GENETICS INST INC.

XX Donaldson DD, Unger MJ, Young DA, Whitters MJ, Lowe L, Collins M;
 PI WPI: 2002-062239/08.

XX N-PSDB; AAS17248.

XX New polypeptide, useful for identifying compounds binding to MU-1, and
 FT for treating multiple sclerosis, rheumatoid arthritis, diabetes and
 FT asthma, comprises the isolated murine MU-1 protein, and a hematopoietin
 FT receptor superfamily chain.

XX Disclosure; Fig 4; 59pp; English.

XX The present invention relates to a new murine MU-1 protein, a
 CC haematopoietin receptor superfamily chain, comprising a fully defined
 CC sequence of 529 amino acids (AAU11915) as given in the specifications or
 CC fragment of protein having MU-1 biological activity. The molecules of the

CC invention may exhibit cytokine, cell proliferation or cell
 CC differentiation activity and may also exhibit immune stimulating or
 CC immune suppressing activity and can be useful in the treatment of various
 CC immune deficiencies and disorders including severe combined
 CC immunodeficiency (SCID). Another use of the invention is treating
 CC autoimmune disorders such as connective tissue disease, multiple
 CC sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune
 CC pulmonary inflammation, autoimmune thyroiditis, insulin dependent
 CC diabetes mellitus, and autoimmune inflammatory eye disease. The invention
 CC is useful for the treatment of myeloid or lymphoid cell deficiencies and
 CC in treating various anemias or for use in conjunction with
 CC irradiation/chemotherapy to stimulate the production of erythroid
 CC precursors and/or erythroid cells. The polynucleotides and proteins can
 CC also be used as nutritional sources or supplements. The present protein
 CC sequence represents the human MU-1 haematopoietin receptor superfamily
 CC chain. MU-1 is also a member of the cytokine receptor family. This
 CC sequence was used in the invention for the characterisation of previously
 CC unknown members of the haematopoietin receptor superfamily

XX Sequence 538 AA;

Query Match 100.0%; Score 1195; DB 5; Length 538;

Best Local Similarity 100.0%; Pred. No. 1.6e-114; Indels 0; Gaps 0;
 Matches 218; Conservative 0; Mismatches 0;

QY 1 CPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY 60
 DB 20 CPDLVCYTDYLTQVICILEMNNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY 79
 QY 61 TCHMDVHFHMADDFISVNTDQSGNSQCGSFLLAESIKPAPPFNVTTFSGQYNISWR 120
 DB 80 TCHMDVHFHMADDFISVNTDQSGNSQCGSFLLAESIKPAPPFNVTTFSGQYNISWR 139
 QY 121 SYDEDPAFYMLKGLQYELQYRNRGDPWAVSPRKLISVDSRSVSLPLEFRKDSSEYELQ 180
 DB 140 SYDEDPAFYMLKGLQYELQYRNRGDPWAVSPRKLISVDSRSVSLPLEFRKDSSEYELQ 199
 QY 181 VRAGPMGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
 DB 200 VRAGPMGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 237

RESULT 12

AAE13726

ID AAE13726 standard; protein; 538 AA.

XX AAE13726;

XX 26-FEB-2002 (first entry)

XX Human soluble Zalphall cytokine receptor protein.

XX Human; Zalphall; cytokine receptor; immunosuppressive; cytostatic;
 KW inflammatory disorder; haemostatic; cell proliferation; immune disorder;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
 KW myasthenia gravis; systemic lupus erythematosus; SLE; diabetes; asthma;
 KW ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis;
 KW viral infection.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..19
 FT /label= Signal_peptide
 FT Protein 20..538
 FT /label= Mature_Zalphall_protein
 FT Domain 20..237
 FT /label= Cytokine_binding_domain
 FT Domain 120..123
 FT /label= Domain_linker
 FT Region 192..202
 FT /notes= "Perultimate strand region"
 FT Domain 214..218

FT	Domain	/note= "WQXWS motif"
FT	238..255	
FT	/label= Transmembrane_domain	
FT	256..538	
FT	/label= Intracellular_signalling_domain	
FT	267..273	
FT	/note= "Box I signalling site"	
FT	301..304	
FT	/note= "Box II signalling site"	
FT	519..522	
FT	/label= STAT3_binding_site	
XX		
XX	WC200177171-A2.	
PN		
XX	18-OCT-2001.	
XX		
PP	03-APR-2001; 2001WO-US010872.	
PP		
PR	05-APR-2000; 2000US-0194731P.	
PR	28-JUL-2000; 2000US-0222121P.	
XX		
XX	(ZYMO) ZYMOGENETICS INC.	
XX		
PI	Sprecher CA, Novak JE, West JW, Presnell SR, Holly RD, Nelson AJ;	
PI	WPI; 2002-025898/03.	
DR	N-PSDB; AAD22918.	
XX		
XX		
PT	Novel soluble receptor polypeptides and polynucleotides used as cytokine	
PT	antagonist for stimulating ligand activity-induced proliferation of	
PT	hematopoietic cells and for suppressing immune response in a mammal.	
XX		
PS	Example 1; Page 172-173; 243pp; English.	
XX		
CC	The invention relates to an isolated soluble zalphall cytokine receptor	
CC	polypeptide and their cDNA molecules. Zalphall proteins are useful for	
CC	inhibiting or antagonising the ligand activity-induced proliferation of	
CC	haematopoietic cells and haematopoietic cell progenitors preferably	
CC	lymphoid cells which are natural killer cells or cytotoxic T cells.	
CC	Zalphall is useful for treating immune and inflammatory disorders, for	
CC	reducing proliferation of neoplastic B or T cells, for suppressing an	
CC	immune response in a mammal exposed to an antigen or pathogen. Zalphall is	
CC	useful for treating diseases that require immune regulation including	
CC	autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,	
CC	myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes;	
CC	asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease,	
CC	sepsis, viral infection (dengue virus infection) and cancer. The present	
CC	sequence is human soluble Zalphall cytokine receptor protein	
XX		
XX		
SQ	Sequence 538 AA;	
	Query Match	100.0%; Score 1195; DB 5; Length 538;
	Best Local Similarity	100.0%; Pred. No. 1.6e-114;
	Matches 218; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	CPDLVCYTDYLTQVTCILEMWNLPSTLTLTWQDYBELKDEATSCSLHRSAAHATHATY 60
DB	20	CPDLVCYTDYLTQVTCILEMWNLPSTLTLTWQDYBELKDEATSCSLHRSAAHATHATY 79
QY	61	TCHMDVHFPMADIDTSVNIITQSGNYSECGSFLLAESIKPAPFNVVTFPGQYNISNR 120
DB	80	TCHMDVHFPMADIDTSVNIITQSGNYSECGSFLLAESIKPAPFNVVTFPGQYNISNR 139
QY	121	SDYEDPAFYMLKGKLYELQYENRGDPWAVSPRKLISVDPSVSLLPLEFRKDSYELQ 180
DB	140	SDYEDPAFYMLKGKLYELQYENRGDPWAVSPRKLISVDPSVSLLPLEFRKDSYELQ 199
QY	181	VRAGPMGSSYQGTSEWSDDPVIFQTQSEELKEGWNPH 218
DB	200	VRAGPMGSSYQGTSEWSDDPVIFQTQSEELKEGWNPH 237

AAU11978	AAU11978 standard; protein; 538 AA.	
ID	AAU11978 standard; protein; 538 AA.	
XX	AAU11978;	
XX	09-APR-2002 (first entry)	
DT	Human zalphall receptor polypeptide.	
XX		
XX	Cytokine; zalphall Ligand; zalphall receptor; NK cell progenitor;	
XX	natural killer cell proliferation; T-cell proliferation;	
KW	B-cell proliferation; anti-tumour response; immune system;	
KW	immunostimulant; cytostatic; human.	
XX		
OS	Homo sapiens.	
XX		
XX	US6307024-B1.	
PN		
PD	23-OCT-2001.	
XX		
XX	09-MAR-2000; 2000US-00522217.	
PF		
XX		
XX	99US-0123547P.	
PR		
XX	11-MAR-1999; 99US-0123904P.	
PR		
XX	01-JUL-1999; 99US-0142013P.	
XX		
XX	(ZYMO) ZYMOGENETICS INC.	
PA		
XX	Novak JE, Presnell JR, Sprecher CA, Foster DC, Holly RD;	
PI	Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;	
PI		
XX		
DR	WFI; 2002-040208/05.	
XX	N-PSDB; AAS20642.	
DR		
XX		
XX	New zalphall ligand polypeptides and polynucleotides, useful for	
PT	stimulating proliferation, activation, differentiation and/or induction	
PT	of inhibition of specialized cell function, or for stimulating an	
PT	antigenic response.	
XX		
XX	Claim 1; Col 191-194; 105pp; English.	
PS		
XX	The present invention relates to the isolation of a novel cytokine,	
XX	zalphall Ligand and the polynucleotide encoding it. The invention also	
CC	gives the sequence for the zalphall receptor and the polynucleotide	
CC	encoding it. The zalphall Ligand polypeptide stimulates proliferation of	
CC	natural killer (NK) cells or NK cell progenitors, the activation of NK	
CC	cells, proliferation of T-cells, proliferation of B-cells stimulated with	
CC	anti-CD40 antibodies, stimulates an antigenic response in a mammal, and	
CC	reduces proliferation of B-cells stimulated with anti-IGM antibodies. The	
CC	zalphall Ligand polypeptide is also useful in preparing antibodies that	
CC	bind to zalphall Ligand epitopes. The zalphall Ligand polynucleotides can	
CC	be used as probes or primers to clone regions of a zalphall Ligand gene,	
CC	and in gene therapy. Zalphall Ligand may also be used to identify	
CC	inhibitors of its activity, to enhance the generation of anti-tumour	
CC	responses with or without the infusion of donor lymphocytes, and to	
CC	activate or stimulate the immune system. The present sequence represents	
CC	human zalphall receptor polypeptide	
XX		
XX	Sequence 538 AA;	
XX		
XX	Query Match 100.0%; Score 1195; DB 5; Length 538;	
XX	Best Local Similarity 100.0%; Pred. NO. 1.6e-114;	
XX	Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
QY	1 CPDLVCYTDYLTQVICILEMWNLFPSLTITLWQDQVEELKDEATSCSLHRSAHNATHATY 60	
DB	20 CPDLVCYTDYLTQVICILEMWNLFPSLTITLWQDQVEELKDEATSCSLHRSAHNATHATY 79	
QY	61 TCHMDVEHFHMADDTFVSNVITDQSGNYSCGCSFLLAESIKPAPPENVTTFSGQYNISWR 120	
DB	80 TCHMDVEHFHMADDTFVSNVITDQSGNYSCGCSFLLAESIKPAPPENVTTFSGQYNISWR 139	
QY	121 SDYEDPAFTYMLKGKLYQELQYLRNGDDFWAPSPRKLISVDSRSVSLLLPFRKDSSELYQ 180	

RESULT 13

Db 140 SYEDPAFYMLKGLQYELQYRNRPDPWAVSPRRKLI SVDRSVSLLEPRKDSSEYELQ 199
 QY 181 VRAGPMPGSSYQGTWSESDPVIFQTSSEELKEGWNPH 218
 Db 200 VRAGPMPGSSYQGTWSESDPVIFQTSSEELKEGWNPH 237

RESULT 14
 ABR61402
 ID ABR61402 standard; protein; 538 AA.
 XX
 AC ABR61402;
 DT 12-AUG-2003 (first entry)
 XX
 DE Human IL-21R SEQ ID NO:2.
 XX
 KW arthritic disorder; interleukin-21; IL-21; IL-21 receptor; IL-21R;
 KW immune cell activity; cancer; infectious disorder; antirheumatic;
 KW antiarthritic; osteopathic; antipsoriatic; cytostatic; antibacterial;
 KW virucide; antiparasitic; immunosuppressive; antidiabetic; dermatological;
 KW neuroprotective; antitumor; antiallergic; antianaemic; hepatotropic;
 KW antithyroid; antinflammatory; immune response; immune disorder;
 KW autoimmune disease; human.
 XX
 OS Homo sapiens.
 PN WC2003028630-A2.
 PD 10-APR-2003.
 XX
 PF 04-OCT-2002; 2002WO-US029839.
 XX
 PR 04-OCT-2001; 2001US-00972218.
 PR 17-APR-2002; 2002US-0373746P.
 XX
 PA (AMHP) WYETH.
 XX
 PI Carter L, Whitters MJ, Collins M, Young DA, Larsen G;
 PI Donaldson DD, Lowe LD, Dunussi K, Ma M, Witek JS, Kasasian MT;
 PI Ungar M;
 XX
 DR WPI; 2003-430146/40.
 DR N-PSDB; ACC80861.
 XX
 PT Treating or preventing arthritic disorder, cancer or infectious disorders
 PT in a subject, involves administering a modulator of interleukin-21 or its
 PT receptor which modulate immune cell activity.
 XX
 PS Claim 40; Fig 2B; 176pp; English.

The invention relates to a novel method for treating or preventing an
 arthritic disorder in a subject. The method involves administering to the
 subject an interleukin-21 (IL-21)/IL-21 receptor (IL-21R) antagonist
 optionally in combination with another therapeutic agent, to inhibit or
 reduce immune cell activity in the subject. The method is also useful for
 treating or preventing cancer or an infectious disorder, in a subject, by
 administering IL-21/IL-21R agonist, to increase immune cell activity. The
 method of the invention has antirheumatic, antiarthritic, osteopathic,
 antipsoriatic, cytostatic, antibacterial, virucide, antiparasitic,
 immunosuppressive, antidiabetic, neuroprotective, dermatological,
 antitumor, antiasthmatic, antiallergic, antianaemic, hepatotropic,
 antithyroid, and antinflammatory activity. The method is useful for
 treating or preventing an arthritic disorder such as rheumatoid
 arthritis, juvenile rheumatoid arthritis, osteoarthritis, psoriatic
 arthritis or ankylosing spondylitis, and also cancer such as solid
 tumour, soft tissue tumour or metastatic lesion, or an infectious
 disorder such as bacterial, viral or parasitic infection in a mammal,
 preferably human. A method of the invention is also useful for
 increasing the ability of a vaccine composition containing an antigen to
 elicit a protective immune response in a subject against the antigens.
 The antigen is from a pathogen such as virus, bacterium or protozoan, or

CC from cancer or tumour cell antigen, or expressed on the surface of cancer
 CC cell. An alternative method of the invention is useful for modulating the
 CC activity of immune or haematopoietic cells and thus to treat or prevent a
 CC variety of immune disorders, such as autoimmune diseases, for example
 CC diabetes mellitus, multiple sclerosis, myasthenia gravis, systemic lupus
 CC erythematosus, dermatitis, ulcer, asthma, allergic asthma, anaemia,
 CC hepatitis, Graves's disease, graft versus host disease, and scleroderma.
 CC The present sequence is used in an exemplification of the invention
 XX
 SQ Sequence 538 AA;

Query Match 100.0%; Score 1195; DB 6; Length 538;
 Best Local Similarity 100.0%; Pred. No. 1.6e-114;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCYTDYLVQVICILEMNLHPSTLTLTWQDYEELEKDEATSCSLHSAHNATHATY 60
 DB 20 CPDLVCYTDYLVQVICILEMNLHPSTLTLTWQDYEELEKDEATSCSLHSAHNATHATY 79
 QY 61 TCHMDVPHFWADDIFSVNITDQSGNYSCGSGFLAESIKPAPPFNVTTFSGQYNISWR 120
 DB 80 TCHMDVPHFWADDIFSVNITDQSGNYSCGSGFLAESIKPAPPFNVTTFSGQYNISWR 139
 QY 121 SYEDPAFYMLKGLQYELQYRNRPDPWAVSPRRKLI SVDRSVSLLEPRKDSSEYELQ 180
 DB 140 SYEDPAFYMLKGLQYELQYRNRPDPWAVSPRRKLI SVDRSVSLLEPRKDSSEYELQ 199
 QY 181 VRAGPMPGSSYQGTWSESDPVIFQTSSEELKEGWNPH 218
 DB 200 VRAGPMPGSSYQGTWSESDPVIFQTSSEELKEGWNPH 237

RESULT 15
 AAE14939
 ID AAE14939 standard; protein; 538 AA.
 XX
 AC AAE14939;
 XX
 DT 27-AUG-2003 (first entry)
 XX
 DE Human interleukin-21 (IL-21) receptor.
 XX
 KW Interleukin-21; antagonist; cancer; inflammatory; autoimmune disorder;
 KW rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus;
 KW myasthenia gravis; diabetes; human; zalfall receptor; IL-21 receptor.
 XX
 OS Homo sapiens.
 PN WC2003040313-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 28-OCT-2002; 2002WO-US034502.
 XX
 PR 05-NOV-2001; 2001US-0337586P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Pressnell SR, West JW, Novak JE;
 XX
 DR WPI; 2003-441547/41.
 DR N-PSDB; AAD47859.
 XX
 PT New IL-21 polypeptide and encoding polynucleotide, useful for diagnosing
 PT and treating disorders with aberrant expression or activity of the IL-21
 PT polypeptide, such as cancer, rheumatoid arthritis, multiple sclerosis and
 PT diabetes.
 XX
 PS Example 1; Page 65-67; 71pp; English.
 XX
 CC The invention relates to polynucleotides and polypeptides of interleukin-
 CC 21 (IL-21) antagonists, that bind with specificity and exhibit an EC50
 CC that is not detectable in receptor binding studies. The antagonists of

CC the invention have mutations in the D helix of the IL-21 molecule, and
CC can be used to inhibit the activity of IL-21 with its cognate receptor.
CC The IL-21 antagonists are useful for diagnosing and treating disorders
CC involving the aberrant expression or activity of the IL-21 polypeptide,
CC such as cancer, inflammatory and autoimmune disorders, including
CC rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,
CC myasthenia gravis and diabetes. The polypeptides can also be used to
CC prepare antibodies that bind IL-21 epitopes, peptides or polypeptides,
CC and for enhancing in vivo killing of target tissues. The present sequence
CC is human IL-21 receptor (originally designated zalphall receptor)
XX
SQ

SQ Sequence 538 AA;

Query Match	100.0%;	Score 1195;	DB 7;	Length 538;
Best Local Similarity	100.0%;	Pred. No. 1.6e-114;		
Matches 218;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CPDLVCYTDYLGQVVICILEMWNLHPSTLTLTWQDQYEELKDEATCSLHRSAHNATHATY	60	
Db	20	CPDLVCYTDYLGQVVICILEMWNLHPSTLTLTWQDQYEELKDEATCSLHRSAHNATHATY	79	
QY	61	TCHMDVHFHMADDFISVNIITDQSGNYSCGSGFLLAESIKPAPPFNVTVTFSGQYNISWR	120	
Db	80	TCHMDVHFHMADDFISVNIITDQSGNYSCGSGFLLAESIKPAPPFNVTVTFSGQYNISWR	139	
QY	121	SDYEDAFYMLKGLQYELQYRNRGDPNAVSPRRKLIISVDSRSVSLPLLEFRKDSSEYELQ	180	
Db	140	SDYEDAFYMLKGLQYELQYRNRGDPNAVSPRRKLIISVDSRSVSLPLLEFRKDSSEYELQ	199	
QY	181	VRAGPMFGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH	218	
Db	200	VRAGPMFGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH	237	

Search completed: March 3, 2004, 12:35:38
Job time : 53.0065 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	1288	100.0	347	1	US-08-052-205-7	Sequence 7, Appli
2	1288	100.0	347	1	US-08-595-974-7	Sequence 7, Appli
3	1288	100.0	369	1	US-08-052-205-4	Sequence 4, Appli
4	1288	100.0	369	1	US-08-595-974-4	Sequence 4, Appli
5	1288	100.0	369	4	US-09-191-786-2	Sequence 20, Appli
6	1288	100.0	691	4	US-09-313-942-20	Sequence 20, Appli
7	1288	100.0	694	4	US-09-313-942-18	Sequence 18, Appli
8	1288	100.0	694	4	US-09-313-942-22	Sequence 22, Appli
9	1282	99.5	482	4	US-09-189-129-2	Sequence 2, Appli
10	1277	98.1	230	1	US-08-052-205-11	Sequence 11, Appli
11	1277	99.1	230	1	US-08-595-974-11	Sequence 11, Appli
12	1277	99.1	252	1	US-08-052-205-9	Sequence 9, Appli
13	1277	99.1	252	1	US-08-595-974-9	Sequence 9, Appli
14	853.5	66.3	369	2	US-08-424-224-2	Sequence 2, Appli
15	853.5	66.3	369	5	PCR-US94-02891-69	Sequence 69, Appli
16	207	16.1	380	1	US-08-609-572-4	Sequence 4, Appli
17	207	16.1	380	3	US-08-841-751-4	Sequence 4, Appli
18	207	16.1	380	3	US-08-846-340-4	Sequence 4, Appli
19	207	16.1	380	3	US-08-846-344-4	Sequence 4, Appli
20	207	16.1	380	4	US-09-301-808-4	Sequence 4, Appli
21	199.5	15.5	383	1	US-08-609-572-2	Sequence 2, Appli
22	199.5	15.5	383	3	US-08-841-751-2	Sequence 2, Appli
23	199.5	15.5	383	3	US-08-846-340-2	Sequence 2, Appli
24	199.5	15.5	383	3	US-08-846-344-2	Sequence 2, Appli
25	199.5	15.5	383	4	US-09-301-808-2	Sequence 2, Appli
26	178	13.8	427	3	US-08-969-125-9	Sequence 9, Appli
27	178	13.8	427	4	US-09-313-942-30	Sequence 30, Appli

Query Match 100.0%; Score 1288; DB 1; Length 347;
Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTILTPNGEDTTADFFLTMTPTDLSVSTPLPPEVQCFVFNVEYMNCTWNSSEPPQ 60
DB 1 LNTTILTPNGEDTTADFFLTMTPTDLSVSTPLPPEVQCFVFNVEYMNCTWNSSEPPQ 60

QY 61 TNLTLHYWTKNSDNDKVKCKSHYLFSEETSCQLOKKEIHLVQYRTDWDHSTEQSV 120
DB 61 TNLTLHYWTKNSDNDKVKCKSHYLFSEETSCQLOKKEIHLVQYRTDWDHSTEQSV 120

QY 121 TQMLKQLNVLIPWAPENLTLHKLSEQLNWNRRFLNHCLEHLVQYRTDWDHSTEQSV 180
DB 121 TQMLKQLNVLIPWAPENLTLHKLSEQLNWNRRFLNHCLEHLVQYRTDWDHSTEQSV 180

QY 181 DYRHKFSLSVDGQKRYTFRVRSRNPCLGSAQHSWSEHPHWSNTSKEN 232
DB 181 DYRHKFSLSVDGQKRYTFRVRSRNPCLGSAQHSWSEHPHWSNTSKEN 232

RESULT 2
US-08-595-974-7
; Sequence 7, Application US/08595974
; Patent No. 5705608
; GENERAL INFORMATION:
; APPLICANT: SUGAMURA, KAZUO
; APPLICANT: TAKESHITA, TOSHIKAZU
; APPLICANT: ASAO, HIRONOBU
; APPLICANT: NAKAMURA, MASATAKA
; APPLICANT: SHIMAMURA, TOSHIRO
; APPLICANT: SUZUKI, MANABU
; APPLICANT: HAMURO, JUNJI
; TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,974
; FILING DATE: 06-FEB-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/052,205
; FILING DATE: 22-APR-1993
; APPLICATION NUMBER: JP 104947/1992
; FILING DATE: 23-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5705608man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-615-0X
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-595-974-7

Query Match 100.0%; Score 1288; DB 1; Length 347;
Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTILTPNGEDTTADFFLTMTPTDLSVSTPLPPEVQCFVFNVEYMNCTWNSSEPPQ 60
DB 1 LNTTILTPNGEDTTADFFLTMTPTDLSVSTPLPPEVQCFVFNVEYMNCTWNSSEPPQ 60

QY 61 TNLTLHYWTKNSDNDKVKCKSHYLFSEETSCQLOKKEIHLVQYRTDWDHSTEQSV 120
DB 61 TNLTLHYWTKNSDNDKVKCKSHYLFSEETSCQLOKKEIHLVQYRTDWDHSTEQSV 120

QY 121 TQMLKQLNVLIPWAPENLTLHKLSEQLNWNRRFLNHCLEHLVQYRTDWDHSTEQSV 180
DB 121 TQMLKQLNVLIPWAPENLTLHKLSEQLNWNRRFLNHCLEHLVQYRTDWDHSTEQSV 180

QY 181 DYRHKFSLSVDGQKRYTFRVRSRNPCLGSAQHSWSEHPHWSNTSKEN 232
DB 181 DYRHKFSLSVDGQKRYTFRVRSRNPCLGSAQHSWSEHPHWSNTSKEN 232

RESULT 3
US-08-052-205-4
; Sequence 4, Application US/08052205
; Patent No. 5510259
; GENERAL INFORMATION:
; APPLICANT: SUGAMURA, KAZUO
; APPLICANT: TAKESHITA, TOSHIKAZU
; APPLICANT: ASAO, HIRONOBU
; APPLICANT: NAKAMURA, MASATAKA
; APPLICANT: SHIMAMURA, TOSHIRO
; APPLICANT: SUZUKI, MANABU
; APPLICANT: HAMURO, JUNJI
; TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/052,205
; FILING DATE: 19930422
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 104947/1992
; FILING DATE: 23-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5510259man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-615-0X
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-052-205-4

Query Match 100.0%; Score 1288; DB 1; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.5e-118;

Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
DB 23 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 82
QY 61 TNLTHYWKNSDNDKVKQCSHYLPSSEITSGCOLQKKEIHLVQTFVVLQDPRPRQA 120
DB 83 TNLTHYWKNSDNDKVKQCSHYLPSSEITSGCOLQKKEIHLVQTFVVLQDPRPRQA 142
QY 121 TQMLKQLNVLIPWAPENLTLLKLSQLELNNRFLNHCLEHLVQYRTDWDHSWTQSV 180
DB 143 TQMLKQLNVLIPWAPENLTLLKLSQLELNNRFLNHCLEHLVQYRTDWDHSWTQSV 202
QY 181 DYRHKFSPLPSVDGQKRYTFRVRSRNPPLCGSAQHSWSESHPIHWSNTSKEN 232
DB 203 DYRHKFSPLPSVDGQKRYTFRVRSRNPPLCGSAQHSWSESHPIHWSNTSKEN 254

RESULT 4

US-08-595-974-4
; Sequence 4, Application US/08595974
; Patent No. 5705608
; GENERAL INFORMATION:
; APPLICANT: SUGAMURA, KAZUO
; APPLICANT: TAKESHITA, TOSHIKAZU
; APPLICANT: ASAO, HIRONOBU
; APPLICANT: NAKAMURA, MASATAKA
; APPLICANT: SHIMAMURA, TOSHIRO
; APPLICANT: SUZUKI, MANABU
; APPLICANT: HAMURO, JUNJI
; TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,974
; FILING DATE: 06-FEB-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/052,205
; FILING DATE: 22-APR-1993
; APPLICATION NUMBER: JP 104947/1992
; FILING DATE: 23-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5705608man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-615-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-595-974-4

Query Match 100.0%; Score 1288; DB 1; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.5e-118;

Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
DB 23 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 82
QY 61 TNLTHYWKNSDNDKVKQCSHYLPSSEITSGCOLQKKEIHLVQTFVVLQDPRPRQA 120
DB 83 TNLTHYWKNSDNDKVKQCSHYLPSSEITSGCOLQKKEIHLVQTFVVLQDPRPRQA 142
QY 121 TQMLKQLNVLIPWAPENLTLLKLSQLELNNRFLNHCLEHLVQYRTDWDHSWTQSV 180
DB 143 TQMLKQLNVLIPWAPENLTLLKLSQLELNNRFLNHCLEHLVQYRTDWDHSWTQSV 202
QY 181 DYRHKFSPLPSVDGQKRYTFRVRSRNPPLCGSAQHSWSESHPIHWSNTSKEN 232
DB 203 DYRHKFSPLPSVDGQKRYTFRVRSRNPPLCGSAQHSWSESHPIHWSNTSKEN 254

RESULT 5

US-09-191-786-2
; Sequence 2, Application US/09191786
; Patent No. 6372898
; GENERAL INFORMATION:
; APPLICANT: Cacalano, Nicholas A.
; APPLICANT: Johnston, James A.
; TITLE OF INVENTION: Mammalian Protein Variants and Methods
; TITLE OF INVENTION: of Use
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/191,786
; FILING DATE: 11-NOV-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0920
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 852-9196
; TELEFAX: (650) 496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURES:
; NAME/KEY: CDS
; LOCATION: 1..1062
US-09-191-786-2

Query Match 100.0%; Score 1288; DB 4; Length 369;

Best Local Similarity 100.0%; Pred. No. 1.5e-118;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
DB 23 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 82
QY 61 TNLTHYWKNSDNDKVKQCSHYLPSSEITSGCOLQKKEIHLVQTFVVLQDPRPRQA 120

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Db 83 TNLTLHYWYKNSDNDKVKQKSHYLFSEETSGCOLQKKEIHLVQTFVVLQDQPREPRA 142
Qy 121 TOMLKLQNLVWPAPENLTLHLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHWSWTEQSV 180
Db 143 TOMLKLQNLVWPAPENLTLHLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHWSWTEQSV 202
Qy 181 DYRHKPSLPSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSKEN 232
Db 203 DYRHKPSLPSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSKEN 254

RESULT 6
US-09-313-942-20
; Sequence 20, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 691
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-20
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Query Match 100.0%; Score 1288; DB 4; Length 691;
Best Local Similarity 100.0%; Pred. No. 3.6e-118; Indels 0; Gaps 0;
Matches 232; Conservative 0; Mismatches 0;

Qy 1 LNTTILTPNGNEDTTADFFLTMTPTDSLVSSTLPPEVQCFVFNVEYMNCTWNSSEPOP 60
Db 23 LNTTILTPNGNEDTTADFFLTMTPTDSLVSSTLPPEVQCFVFNVEYMNCTWNSSEPOP 82
Qy 61 TNLTLHYWYKNSDNDKVKQKSHYLFSEETSGCOLQKKEIHLVQTFVVLQDQPREPRA 120
Db 83 TNLTLHYWYKNSDNDKVKQKSHYLFSEETSGCOLQKKEIHLVQTFVVLQDQPREPRA 142
Qy 121 TOMLKLQNLVWPAPENLTLHLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHWSWTEQSV 180
Db 143 TOMLKLQNLVWPAPENLTLHLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHWSWTEQSV 202
Qy 181 DYRHKPSLPSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSKEN 232
Db 203 DYRHKPSLPSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSKEN 254
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RESULT 7
US-09-313-942-18
; Sequence 18, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 18
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-18

Query Match 100.0%; Score 1288; DB 4; Length 694;
Best Local Similarity 100.0%; Pred. No. 3.6e-118; Indels 0; Gaps 0;
Matches 232; Conservative 0; Mismatches 0;

Qy 1 LNTTILTPNGNEDTTADFFLTMTPTDSLVSSTLPPEVQCFVFNVEYMNCTWNSSEPOP 60
Db 23 LNTTILTPNGNEDTTADFFLTMTPTDSLVSSTLPPEVQCFVFNVEYMNCTWNSSEPOP 82
Qy 61 TNLTLHYWYKNSDNDKVKQKSHYLFSEETSGCOLQKKEIHLVQTFVVLQDQPREPRA 120
Db 83 TNLTLHYWYKNSDNDKVKQKSHYLFSEETSGCOLQKKEIHLVQTFVVLQDQPREPRA 142
Qy 121 TOMLKLQNLVWPAPENLTLHLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHWSWTEQSV 180
Db 143 TOMLKLQNLVWPAPENLTLHLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHWSWTEQSV 202
Qy 181 DYRHKPSLPSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSKEN 232
Db 203 DYRHKPSLPSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSKEN 254

RESULT 8
US-09-313-942-22
; Sequence 22, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-22
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Query Match 100.0%; Score 1288; DB 4; Length 694;
Best Local Similarity 100.0%; Pred. No. 3.6e-118; Indels 0; Gaps 0;
Matches 232; Conservative 0; Mismatches 0;

Qy 1 LNTTILTPNGNEDTTADFFLTMTPTDSLVSSTLPPEVQCFVFNVEYMNCTWNSSEPOP 60
Db 23 LNTTILTPNGNEDTTADFFLTMTPTDSLVSSTLPPEVQCFVFNVEYMNCTWNSSEPOP 82
Qy 61 TNLTLHYWYKNSDNDKVKQKSHYLFSEETSGCOLQKKEIHLVQTFVVLQDQPREPRA 120
Db 83 TNLTLHYWYKNSDNDKVKQKSHYLFSEETSGCOLQKKEIHLVQTFVVLQDQPREPRA 142
Qy 121 TOMLKLQNLVWPAPENLTLHLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHWSWTEQSV 180
Db 143 TOMLKLQNLVWPAPENLTLHLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHWSWTEQSV 202
Qy 181 DYRHKPSLPSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSKEN 232
Db 203 DYRHKPSLPSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSKEN 254
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```
RESULT 9
US-09-189-129-2
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; Sequence 2, Application US/09189129
; Patent No. 6323027
; GENERAL INFORMATION:
; APPLICANT: Burkly, Linda C
; APPLICANT: Benjamin, Christopher D
; APPLICANT: Hession, Catherine A
; APPLICANT: Whitty, Adrian
; TITLE OF INVENTION: COMMON GAMMA CHAIN BLOCKING AGENTS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/189,129
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: A006 PCT CIP
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 60/017,466
; FILING DATE: 10-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A006 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 679-2000
; TELEFAX: 617 679-2838
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 482 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
US-09-189-129-2

Query Match 99.5%; Score 1282; DB 4; Length 482;
Best Local Similarity 99.6%; Pred. No. 8.4e-118;
Matches 231; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LNTTILTPNGNEDTTADPFLTMTDLSLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
DB 23 LNTTILTPNGNEDTTADPFLTMTDLSLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 82
QY 61 TNLTLHYWYKNSDNDKVKQKSHYLFSEITSGCQLOKKEIHLVQTFVYVQLQDPREPRQA 120
DB 83 TNLTLHYWYKNSDNDKVKQKSHYLFSEITSGCQLOKKEIHLVQTFVYVQLQDPREPRQA 142
QY 121 TOMLKLQNLVWPAPENLTLLKLSQLELANNRFLNCHLEHLVQYRTDWDHSHWTEQSV 180
DB 143 TOMLKLQNLVWPAPENLTLLKLSQLELANNRFLNCHLEHLVQYRTDWDHSHWTEQSV 202
QY 181 DYRHKFSLPSVDGQKRYTFRVRSRNPPLCGSAQHWSEWSHPHIGWSNTSKN 232
DB 203 DYRHKFSLPSVDGQKRYTFRVRSRNPPLCGSAQHWSEWSHPHIGWSNTSKN 254

RESULT 10
US-08-052-205-11
; Sequence 11, Application US/08052205
; Patent No. 5510259
; GENERAL INFORMATION:

; APPLICANT: SUGAMURA, KAZUO
; APPLICANT: TAKESHITA, TOSHIKAZU
; APPLICANT: ASAO, HIRONOBU
; APPLICANT: NAKAMURA, MASATAKA
; APPLICANT: SHIMAMURA, TOSHIRO
; APPLICANT: SUZUKI, MANABU
; APPLICANT: HAMURO, JUNJI
; TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/052,205
; FILING DATE: 19930422
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 104947/1992
; FILING DATE: 23-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5510259man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-615-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-052-205-11

Query Match 99.1%; Score 1277; DB 1; Length 230;
Best Local Similarity 100.0%; Pred. No. 9.2e-118;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNTTILTPNGNEDTTADPFLTMTDLSLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
DB 1 LNTTILTPNGNEDTTADPFLTMTDLSLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
QY 61 TNLTLHYWYKNSDNDKVKQKSHYLFSEITSGCQLOKKEIHLVQTFVYVQLQDPREPRQA 120
DB 61 TNLTLHYWYKNSDNDKVKQKSHYLFSEITSGCQLOKKEIHLVQTFVYVQLQDPREPRQA 120
QY 121 TOMLKLQNLVWPAPENLTLLKLSQLELANNRFLNCHLEHLVQYRTDWDHSHWTEQSV 180
DB 121 TOMLKLQNLVWPAPENLTLLKLSQLELANNRFLNCHLEHLVQYRTDWDHSHWTEQSV 180
QY 181 DYRHKFSLPSVDGQKRYTFRVRSRNPPLCGSAQHWSEWSHPHIGWSNTSK 230
DB 181 DYRHKFSLPSVDGQKRYTFRVRSRNPPLCGSAQHWSEWSHPHIGWSNTSK 230

RESULT 11
US-08-595-974-11
; Sequence 11, Application US/08595974
; Patent No. 5705608
; GENERAL INFORMATION:
; APPLICANT: SUGAMURA, KAZUO
; APPLICANT: TAKESHITA, TOSHIKAZU

APPLICANT: ASAO, HIRONOBU
APPLICANT: NAKAMURA, MASATAKA
APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: SUZUKI, MANABU
APPLICANT: HAMURO, JUNJI
TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,974
FILING DATE: 06-FEB-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/052,205
FILING DATE: 22-APR-1993
APPLICATION NUMBER: JP 104947/1992
FILING DATE: 23-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 570560man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-615-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-595-974-11

Query Match 99.1%; Score 1277; DB 1; Length 230;
Best Local Similarity 100.0%; Pred. No. 9.2e-118; Mismatches 0; Indels 0; Gaps 0;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNTTLTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
Db 1 LNTTLTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
QY 61 TNLTLHWYKNSDNDKVKQCSHYLPFSEETSGCQKKEIHLVQYTFVVLQDPREPRAQ 120
Db 61 TNLTLHWYKNSDNDKVKQCSHYLPFSEETSGCQKKEIHLVQYTFVVLQDPREPRAQ 120
QY 121 TQMLKQLNVLIPWAPENLTLHLKLSQLELNWNNRFLNHLVQYRTDWDHWSWTEQSV 180
Db 121 TQMLKQLNVLIPWAPENLTLHLKLSQLELNWNNRFLNHLVQYRTDWDHWSWTEQSV 180
QY 181 DYRHKESLPVDCQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSK 230
Db 181 DYRHKESLPVDCQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSK 230

RESULT 12
US-08-595-974-9
Sequence 9, Application US/08052205
Patent No. 5510259
GENERAL INFORMATION:
APPLICANT: SUGAMURA, KAZUO
APPLICANT: TAKESHITA, TOSHIKAZU

APPLICANT: ASAO, HIRONOBU
APPLICANT: NAKAMURA, MASATAKA
APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: SUZUKI, MANABU
APPLICANT: HAMURO, JUNJI
TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/052,205
FILING DATE: 19930422
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 104947/1992
FILING DATE: 23-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5510259man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-615-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-052-205-9
Query Match 99.1%; Score 1277; DB 1; Length 252;
Best Local Similarity 100.0%; Pred. No. 1e-117; Mismatches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNTTLTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
Db 23 LNTTLTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 82
QY 61 TNLTLHWYKNSDNDKVKQCSHYLPFSEETSGCQKKEIHLVQYTFVVLQDPREPRAQ 120
Db 83 TNLTLHWYKNSDNDKVKQCSHYLPFSEETSGCQKKEIHLVQYTFVVLQDPREPRAQ 142
QY 121 TQMLKQLNVLIPWAPENLTLHLKLSQLELNWNNRFLNHLVQYRTDWDHWSWTEQSV 180
Db 143 TQMLKQLNVLIPWAPENLTLHLKLSQLELNWNNRFLNHLVQYRTDWDHWSWTEQSV 202
QY 181 DYRHKESLPVDCQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSK 230
Db 203 DYRHKESLPVDCQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSK 252

RESULT 13
US-08-595-974-9
Sequence 9, Application US/08595974
Patent No. 5705608
GENERAL INFORMATION:
APPLICANT: SUGAMURA, KAZUO
APPLICANT: TAKESHITA, TOSHIKAZU
APPLICANT: ASAO, HIRONOBU
APPLICANT: NAKAMURA, MASATAKA

APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: SUZUKI, MANABU
APPLICANT: HAMURO, JUNJI
TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C. Jefferson Davis Highway, Suite 400
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,974
FILING DATE: 06-FEB-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/052,205
FILING DATE: 22-APR-1993
APPLICATION NUMBER: JP 104947/1992
FILING DATE: 23-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5705608man P.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-615-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-595-974-9

Query Match 99.1%; Score 1277; DB 1; Length 252;
Best Local Similarity 100.0%; Pred. No. 1e-117;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTILTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFFVNFVYMNCTWNSSEPOQ 60
DB 23 LNTTILTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFFVNFVYMNCTWNSSEPOQ 82
QY 61 TNLTLHYWYKNSDNDKVQKSHYLFSEBITSGCOLQKKEIHLVYQTFVVLQDPREPRQA 120
DB 83 TNLTLHYWYKNSDNDKVQKSHYLFSEBITSGCOLQKKEIHLVYQTFVVLQDPREPRQA 142
QY 121 TOMLKLQNLVLPWAPENLTJLHKLSEQLNANNRFLNHCLEHLVQYRTDWDHSHWTQSV 180
DB 143 TOMLKLQNLVLPWAPENLTJLHKLSEQLNANNRFLNHCLEHLVQYRTDWDHSHWTQSV 202
QY 181 DYRHKFLSPVDGQKRYTFRVRSRFPNPLCGSAQHSWSESHPIHWSNTSK 230
DB 203 DYRHKFLSPVDGQKRYTFRVRSRFPNPLCGSAQHSWSESHPIHWSNTSK 252

RESULT 14
US-08-424-224-2
; Sequence 2, Application US/08424224
; Patent No. 5912173
; GENERAL INFORMATION:
; APPLICANT: LEONARD, WARREN J.
; TITLE OF INVENTION: MURINE IL-2R CDNA AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVE.
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,224
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/121,435
FILING DATE: 14-SEPT-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4061US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 369
TYPE: AMINO ACID
TOPOLOGY: UNKNOWN
MOLECULE TYPE:
DESCRIPTION: PROTEIN
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: MURINE
INDIVIDUAL ISOLATE: IL-2R
US-08-424-224-2

Query Match 66.3%; Score 853.5; DB 2; Length 369;
Best Local Similarity 67.2%; Pred. No. 8e-76;
Matches 156; Conservative 33; Mismatches 42; Indels 1; Gaps 1;

QY 2 NVTTLTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFFVNFVYMNCTWNSSEPOQ 61
DB 24 SSKVLMSSANEDIKADLILTSTAPEHLSAPTLPPEVQCFFVNFVYMNCTWNSSEPOQ 83
QY 62 NLTLYWYKNSDNDKVQKSHYLFSEBITSGCOLQKKEIHLVYQTFVVLQDPREPRQA 121
DB 84 NLTLYWYKNSDNDKVQKSHYLFSEBITSGCOLQKKEIHLVYQTFVVLQDPREPRQA 143
QY 122 QMLKLQNLVLPWAPENLTJLHKLSEQLNANNRFLNHCLEHLVQYRTDWDHSHWTQSV 180
DB 144 QMLKLQNLVLPWAPENLTJLHKLSEQLNANNRFLNHCLEHLVQYRTDWDHSHWTQSV 203
QY 181 DYRHKFLSPVDGQKRYTFRVRSRFPNPLCGSAQHSWSESHPIHWSNTSKEN 232
DB 204 NHEPFLSPVDLAKRYTFRVRSRFPNPLCGSAQHSWSESHPIHWSNTSKEN 255

RESULT 15
PCT-US94-02891-69
; Sequence 69, Application PC/TUS9402891
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN
; APPLICANT: SERVICES
; APPLICANT: OFFICE OF TECHNOLOGY TRANSFER, NATIONAL
; APPLICANT: INSTITUTES OF HEALTH, BOX OTT, BETHESDA, MARYLAND 20892 USA
; TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: XSCID
; NUMBER OF SEQUENCES: 69

Search completed: March 3, 2004, 12:39:55
Job time : 17.3007 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 3, 2004, 12:25:04 ; Search time 8.71896 Seconds
(without alignments)
1385.519 Million cell updates/sec

Title: US-09-825-561A-4

Perfect score: 1288

Sequence: 1 LNTLTTPNGNEDTTADFFL.....QHWSEWSPTHWGSNTSKEN 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1288	100.0	369	1	CYRG HUMAN
2	1097	85.2	373	1	CYRG CANFA
3	990.5	76.9	379	1	CYRG BOVIN
4	853.5	66.3	369	1	CYRG MOUSE
5	207	16.1	380	1	1132 HUMAN
6	181.5	14.1	424	1	1131 MOUSE
7	178	13.8	427	1	1131 HUMAN
8	159.5	12.4	371	1	CEL2 HUMAN
9	159	12.3	897	1	CYRB HUMAN
10	150	11.6	831	1	PRLR CHICK
11	146.5	11.4	400	1	GMCR HUMAN
12	145.5	11.3	831	1	PRLR MELGA
13	132.5	10.3	830	1	PRLR COLLI
14	132	10.2	810	1	IL4B MOUSE
15	125	9.7	896	1	CYRB BOVIN
16	121.5	9.4	581	1	PRLR BOVIN
17	120	9.3	538	1	121R HUMAN
18	118	9.2	415	1	IL5R MOUSE
19	117.5	9.1	359	1	C8ci19 MOUSE
20	116	9.0	878	1	113B MOUSE
21	114	8.9	360	1	CEL2 RAT
22	114	8.9	460	1	IL6A MOUSE
23	113	8.8	581	1	PRLR CEREL
24	112	8.7	420	1	IL5R HUMAN
25	112	8.7	918	1	IL6B HUMAN
26	110.5	8.6	551	1	IL2B HUMAN
27	109.5	8.5	608	1	PRLR MOUSE
28	109	8.5	462	1	IL6A RAT
29	108.5	8.4	610	1	PRLR RAT
30	106	8.2	581	1	PRLR SHEEP
31	105	8.2	539	1	IL2B MOUSE
32	105	8.2	1356	1	CA21 ONCMY
33	104.5	8.1	917	1	IL6B MOUSE

34	104	8.1	1493	1	NEO1 MOUSE
35	102	7.9	611	1	GHR COLLI
36	100	7.8	529	1	121R MOUSE
37	98.5	7.6	918	1	IL6B RAT
38	97.5	7.6	467	1	IL6A PIG
39	97.5	7.6	608	1	GHR CHICK
40	97.5	7.6	825	1	IL4R HUMAN
41	96.5	7.5	625	1	TPOR MOUSE
42	95.5	7.4	622	1	PRLR HUMAN
43	95.5	7.4	630	1	PRLR ORENI
44	95.5	7.4	1461	1	NEO1 HUMAN
45	95	7.4	312	1	F3ST_FLABI

ALIGNMENTS

RESULT 1

ID	CYRG HUMAN	STANDARD;	PRT;	369 AA.
AC	P31785;			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Cytokine receptor common gamma chain precursor (Gamma-C) (Interleukin-2 receptor gamma chain) (IL-2R gamma chain) (P64) (CD132 antigen).			
GN	IL2RG.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]_TaxID=9606;			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RX	MEDLINE=92335883; PubMed=1631559;			
RA	Takeshita T., Asao H., Ohtani K., Ishii N., Kumaki S., Tanaka N.,			
RA	Munakata H., Nakamura M., Sugamura K.;			
RT	"Cloning of the gamma chain of the human IL-2 receptor.";			
RL	Science 257:379-382(1992).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=92393887; PubMed=8514792;			
RA	Noguchi M., Adelstein S., Cao X., Leonard W.J.;			
RT	"Characterization of the human interleukin-2 receptor gamma chain gene.";			
RL	J. Biol. Chem. 268:13601-13608(1993).			
RN	[3]			
RP	SEQUENCE FROM N.A., AND VARIANTS XSCID ASP-114 AND ASN-153.			
RX	MEDLINE=94004847; PubMed=8401490;			
RA	Fuck J.M., Deschenes S.M., Porter J.C., Dutra A.S., Brown C.J.,			
RA	Willard H., Henthorn P.S.;			
RT	"The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated in X-linked severe combined immunodeficiency, SCIDX1.";			
RL	Hum. Mol. Genet. 2:1099-1104(1993).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=B-cell;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Munz D.W., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [5]
 RP IDENTIFICATION AS A IL-4R SUBUNIT.
 RX MEDLINE=94090315; PubMed=8266076;
 RA Kondo M., Takeshita T., Ishii N., Nakamura M., Watanabe S.,
 RA Arai K.-I., Sugamura K.,
 RT "Sharing of the interleukin-2 (IL-2) receptor gamma chain between
 receptors for IL-2 and IL-4.";
 RL Science 262:1874-1877 (1993).
 RN [6]
 RP IDENTIFICATION AS A IL-4R SUBUNIT.
 RX MEDLINE=94090317; PubMed=8266078;
 RA Russell S.M., Kegan A.D., Harada N., Nakamura Y., Noguchi M.,
 RA Leland P., Friedmann M.C., Miyajima A., Puri R.K., Paul W.E.,
 RA Leonard W.J.,
 RT "Interleukin-2 receptor gamma chain: a functional component of the
 interleukin-4 receptor.";
 RL Science 262:1880-1883 (1993).
 RN [7]
 RP IDENTIFICATION AS A IL-7R SUBUNIT.
 RX MEDLINE=94090316; PubMed=8266077;
 RA Noguchi M., Nakamura Y., Russell S.M., Ziegler S.F., Tsang M., Cao X.,
 RA Leonard W.J.,
 RT "Interleukin-2 receptor gamma chain: a functional component of the
 interleukin-7 receptor.";
 RL Science 262:1877-1880 (1993).
 RN [8]
 RP 3D-STRUCTURE MODELING OF 57-248.
 RX MEDLINE=95111955; PubMed=7529123;
 RA Bamorough P., Hedgecock C.J., Richards W.G.,
 RA "The interleukin-2 and interleukin-4 receptors studied by molecular
 modelling.";
 RL Structure 2:839-851 (1994).
 RN [9]
 RP VARIANTS XSCID PHE-115; CYS-240 AND ILE-241.
 RX MEDLINE=94130970; PubMed=8299698;
 RA Disanto J.P., Dautry-Varsat A., Certain S., Fischer A.,
 RA de Saint Basile G.,
 RT "Interleukin-2 (IL-2) receptor gamma chain mutations in X-linked
 severe combined immunodeficiency disease result in the loss of
 high-affinity IL-2 receptor binding.";
 RL Eur. J. Immunol. 24:475-479 (1994).
 RN [10]
 RP VARIANT XSCID LYS-68.
 RX MEDLINE=94375038; PubMed=8088810;
 RA Markiewicz S., Subtil A., Dautry-Varsat A., Fischer A.,
 RA de Saint Basile G.,
 RT "Detection of three nonsense mutations and one missense mutation in
 the interleukin-2 receptor gamma chain gene in SCIDx1 that
 differently affect the mRNA processing.";
 RL Genomics 21:291-293 (1994).
 RN [11]
 RP VARIANT XSCID HIS-162.
 RX MEDLINE=94300093; PubMed=8027558;
 RA Ishii N., Asao H., Kimura Y., Takeshita T., Nakamura M., Tsuchiya S.,
 RA Konno T., Maeda M., Uchiyama T., Sugamura K.,
 RT "Impairment of ligand binding and growth signaling of mutant IL-2
 receptor gamma-chains in patients with X-linked severe combined
 immunodeficiency.";
 RL J. Immunol. 153:1310-1317 (1994).
 RN [12]
 RP VARIANT XSCID ASN-39.
 RX MEDLINE=95023932; PubMed=7937790;
 RA Disanto J.P., Rieux-Laucat F., Dautry-Varsat A., Fischer A.,
 RA de Saint Basile G.,
 RT "Defective human interleukin 2 receptor gamma chain in an atypical X
 chromosome-linked severe combined immunodeficiency with peripheral T
 cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:9466-9470 (1994).

RN [13]
 RP VARIANTS XSCID CYS-226 AND HIS-226.
 RX MEDLINE=95397841; PubMed=7668284;
 RA Pepper A.E., Buckley R.H., Small T.N., Puck J.M.,
 RT "Two mutational hotspots in the interleukin-2 receptor gamma chain
 gene causing human X-linked severe combined immunodeficiency.";
 RL Am. J. Hum. Genet. 57:564-571 (1995).
 RN [14]
 RP VARIANT XSCID SER-183.
 RX MEDLINE=96013903; PubMed=7557965;
 RA Clark P.A., Lester T., Genet S., Jones A.M., Hendriks R.,
 RA Lavinsky R.L., Kinnon C.,
 RT "Screening for mutations causing X-linked severe combined
 immunodeficiency in the IL-2R gamma chain gene by single-strand
 conformation polymorphism analysis.";
 RL Hum. Genet. 96:427-432 (1995).
 RN [15]
 RP VARIANT XSCID GLN-HIS-TRP-237 INS.
 RX MEDLINE=95164726; PubMed=7860773;
 RA Puck J.M., Pepper A.E., Bedard P.-M., Laframboise R.,
 RT "Female germ line mosaicism as the origin of a unique IL-2 receptor
 gamma-chain mutation causing X-linked severe combined
 immunodeficiency.";
 RL J. Clin. Invest. 95:895-899 (1995).
 RN [16]
 RP VARIANT XSCID GLN-293.
 RX MEDLINE=95190013; PubMed=7893965;
 RA Schmaisteg F.C., Leonard W.J., Noguchi M., Berg M., Rudloff H.E.,
 RA Denney R.M., Dave S.K., Brooks E.G., Goldman A.S.,
 RT "Missense mutation in exon 7 of the common gamma chain gene causes a
 moderate form of X-linked combined immunodeficiency.";
 RL J. Clin. Invest. 95:1169-1173 (1995).
 RN [17]
 RP VARIANT XSCID ARG-115.
 RX MEDLINE=97042245; PubMed=8900089;
 RA Stephan V., Wann V., Le Deist F., Dirksen U., Broeker B.,
 RA Mueller-Fleckenstein I., Horneff G., Schroten H., Fischer A.,
 RA de Saint Basile G.,
 RT "Atypical X-linked severe combined immunodeficiency due to possible
 spontaneous reversion of the genetic defect in T cells.";
 RL New Engl. J. Med. 335:1563-1567 (1996).
 RN [18]
 RP VARIANT XSCID GLN-285.
 RX MEDLINE=97295088; PubMed=9150740;
 RA Jones A.M., Clark P.A., Katz F., Genet S., McMahon C., Alterman L.,
 RA Cant A., Kinnon C.,
 RT "B-cell-negative severe combined immunodeficiency associated with a
 common gamma chain mutation.";
 RL Hum. Genet. 99:677-680 (1997).
 RN [19]
 RP VARIANT XSCID CYS-222.
 RX MEDLINE=98064061; PubMed=9399950;
 RA Sharfe N., Shahar M., Roifman C.M.,
 RT "An interleukin-2 receptor gamma chain mutation with normal thymus
 morphology.";
 RL J. Clin. Invest. 100:3036-3043 (1997).
 RN [20]
 RP FUNCTION: Common subunit for the receptors for a variety of
 interleukins.
 CC -1- SUBUNIT: The gamma chain is common to the IL2, IL4, IL7, IL21 and
 probably also the IL13 receptors.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DISEASE: Defects in IL2RG are the cause of X-linked severe
 combined immunodeficiency (XSCID) [MIM:300400]; also known as
 agammaglobulinemia, Swiss type.
 CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors.
 CC Subfamily 5.
 CC -1- SIMILARITY: Contains 1 fibronectin type III domain.
 CC -1- DATABASE: NMBP=PROW; NOTE=CD guide CD132 entry;
 WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd132.htm".
 CC -1- DATABASE: NMBP=IL2RGbase; NOTE=X-linked SCID mutation database;
 WWW="http://www.hgri.nih.gov/DIR/GMB8/SCID/".
 CC -----
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Query Match 100.0%; Score 1288; DB 1; Length 369;
 Best Local Similarity 100.0%; Pred. No. 3.9e-99;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTLTLPNGNEDTADFFLTMTDLSVSTPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
 DB 23 LNTLTLPNGNEDTADFFLTMTDLSVSTPLPEVQCFVFNVEYMNCTWNSSEPPQ 82

QY 61 TNLTHWYKNSDNDKVKQKSHYLFSEITSGCQLOKKEIHLVQTFVVLQODPREP 120
 DB 83 TNLTHWYKNSDNDKVKQKSHYLFSEITSGCQLOKKEIHLVQTFVVLQODPREP 142

QY 121 TQMLKQLNVLIPWAPENLTLLKSESQLELNWNNRFLNHCLHLEHLVQVTDWHSWTEQSV 180
 DB 143 TQMLKQLNVLIPWAPENLTLLKSESQLELNWNNRFLNHCLHLEHLVQVTDWHSWTEQSV 202

QY 181 DYRKHFSLPSVDGQKRYTFRVRSFNPCLGSAQHSWSESHPIHWGNTSKEN 232
 DB 203 DYRKHFSLPSVDGQKRYTFRVRSFNPCLGSAQHSWSESHPIHWGNTSKEN 254

RESULT 2

CYRG CANFA STANDARD; PRT; 373 AA.

AC P40321, 1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cytokine receptor common gamma chain precursor (Gamma-C)
 DE (Interleukin-2 receptor gamma chain) (IL-2R gamma chain) (P64).
 EN IL2RG.
 DS Canis familiaris (Dog).
 DC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 DX NCBI_TaxID=9615;
 [1]
 SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=95130114; PubMed=7829104;
 RA Henthorn P.S.; Somberg R.L.; Fimiani V.M.; Puck J.M.; Patterson D.F.,
 Felsburg P.J.;
 RT "IL-2R gamma gene microdeletion demonstrates that canine X-linked
 RT severe combined immunodeficiency is a homologue of the human
 RT disease.";
 RL Genomics 23:69-74 (1994).
 CC -!- FUNCTION: Common subunit for the receptors for a variety of
 CC interleukins.
 CC -!- SUBUNIT: The gamma chain is common to the IL2, IL4, IL7, IL21 and
 CC probably also the IL13 receptors.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- DISEASE: Defects in IL2RG are the cause of a canine X-linked
 CC severe combined immunodeficiency.
 CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
 CC Subfamily 5.
 CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
 CC
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 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL; U04361; AAC48403.1; --
 DR PIR; A55718; A55718.
 DR HGSP; P31785; 11LM.
 DR InterPro; IPR002996; CR1A.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR003531; Hemtopoptn_S_F1.
 DR SMART; SM00060; FN3; 1.

DR PROSITE; PS01355; HEMATOPO REC S_F1; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 373
 FT DOMAIN 23 261
 FT TRANSMEM 262 283
 FT DOMAIN 284 373
 FT DOMAIN 151 249
 FT DISULFID 62 72
 FT DISULFID 102 115
 FT CARBOHYD 24 24
 FT CARBOHYD 71 71
 FT CARBOHYD 75 75
 FT CARBOHYD 84 84
 FT CARBOHYD 159 159
 FT CARBOHYD 164 164
 FT CARBOHYD 249 249
 SQ SEQUENCE 373 AA; 42516 MW; 03A0DE1F8B089DBB CRC64;

Query Match 85.2%; Score 1097; DB 1; Length 373;

Best Local Similarity 82.8%; Pred. No. 2.3e-83;
 Matches 192; Conservative 24; Mismatches 16; Indels 0; Gaps 0;

QY 1 LNTLTLPNGNEDTADFFLTMTDLSVSTPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
 DB 23 LNSTVPMENGEDITPDFFLTATPSETLSVSSPLPEVQCFVFNVEYMNCTWNSSEPPQ 82

QY 61 TNLTHWYKNSDNDKVKQKSHYLFSEITSGCQLOKKEIHLVQTFVVLQODPREP 120
 DB 83 TNLTHWYKNSDNDKVKQKSHYLFSEITSGCQLOKKEIHLVQTFVVLQODPREP 142

QY 121 TQMLKQLNVLIPWAPENLTLLKSESQLELNWNNRFLNHCLHLEHLVQVTDWHSWTEQSV 180
 DB 143 TQMLKQLNVLIPWAPENLTLLKSESQLELNWNNRFLNHCLHLEHLVQVTDWHSWTEQSV 202

QY 181 DYRKHFSLPSVDGQKRYTFRVRSFNPCLGSAQHSWSESHPIHWGNTSKEN 232
 DB 203 DYRKHFSLPSVDGQKRYTFRVRSFNPCLGSAQHSWSESHPIHWGNTSKEN 254

RESULT 3

CYRG BOVIN STANDARD; PRT; 379 AA.

AC Q95118;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cytokine receptor common gamma chain precursor (Gamma-C)
 DE (Interleukin-2 receptor gamma chain) (IL-2R gamma chain) (P64).
 GN IL2RG.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96268473; PubMed=8672241;
 RA Yoo J., Stone R.T., Solinas-Toldo S., Fries R., Beattie C.W.;
 RT "Cloning and chromosomal mapping of bovine interleukin-2 receptor
 RT gamma gene.";
 RL DNA Cell Biol. 15:453-459 (1996).
 CC -!- FUNCTION: Common subunit for the receptors for a variety of
 CC interleukins.
 CC -!- SUBUNIT: The gamma chain is common to the IL2, IL4, IL7, IL21 and
 CC probably also the IL13 receptors.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
 CC Subfamily 5.
 CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
 CC
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 CC
 CC EMBL; U04361; AAC48403.1; --
 DR PIR; A55718; A55718.
 DR HGSP; P31785; 11LM.
 DR InterPro; IPR002996; CR1A.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR003531; Hemtopoptn_S_F1.
 DR SMART; SM00060; FN3; 1.

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CC -----
 DR EMBL; U33748; AAB07812.1; -
 DR HSSP; F31785; IILM.
 DR InterPro; IPR002996; CRIA.
 DR InterPro; IPR008957; FN III-like.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR003531; Hemtopoptn_s_F1.
 DR Pfam; PF00041; fn3; 1.
 DR SMART; SM00060; FN3; 1.

DR PROSITE; PS01355; HENATOPO_REC_S_F1; 1.
 DR Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 22

FT CHAIN 23 379
 FT DOMAIN 23 269
 FT TRANSMEM 270 290
 FT DOMAIN 291 379
 FT DOMAIN 158 256
 FT DISULFID 68 78
 FT DISULFID 109 122
 FT CARBOHYD 77 77
 FT CARBOHYD 81 81
 FT CARBOHYD 90 90
 FT CARBOHYD 166 166
 FT CARBOHYD 171 171
 SQ SEQUENCE 379 AA; 43037 MW; 33CFAD9C9B032178 CRC64;

Query Match 76.9%; Score 990.5; DB 1; Length 379;
 Best Local Similarity 76.2%; Pred. No. 1.4e-74;
 Matches 182; Conservative 21; Mismatches 29; Indels 7; Gaps 2;

OY 1 LNTTILTPNGED-----TTADFLTTMTDLSVSTLPPEVQCFFVNFVYNCNTWS 54
 DB 23 LNPFLTPSGNEDIGKPGTGDFLTTPAATLDVSTLPKQCFFVNFVYNCNTWS 82
 OY 55 SSEPOTNLTHYWKYK-SNDKVKCKSHYLFSEBITSGCQKKEIHLQYOTFVVQLQDP 113
 DB 83 SSEPQNNLTHYGRNFNGDKLQECGYLFESEITSGCWFGKEIRLYETFFVQLQDP 142
 OY 114 RPRQATQMLKQNLVWPAPENLTHKLSQELNWNRFNLHCLHVLQVTRTDWH 173
 DB 143 RHRKQPKQMLKQDLVWPAPENLTLNLSFQELSNRYLDHCLHVLQVRSRDR 202
 OY 174 SWTEQSDVVRHKFSIPSDGQKRYTFRVRSRNPFLCGSAQHSWSPHIGNSNTSKEN 232
 DB 203 SWTEQSDVHRHSFSLPSVDAAQLYIFRVRSRNPFLCGSAQHSWSPHIGNSNTSKEN 261

RESULT 4
 CYRG_MOUSE STANDARD; PRT; 369 AA.
 AC P34502;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cytokine receptor common gamma chain precursor (Gamma-C)
 DE (Interleukin-2 receptor gamma chain) (IL-2R gamma chain) (P64).
 GN IL2RG.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCB_I_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9327575; PubMed=8503926;
 RA Kumaki S., Kondo M., Takeshita T., Asao H., Nakamura M., Sugamura K.;
 RT "Cloning of the mouse interleukin 2 receptor gamma chain:
 RT demonstration of functional differences between the mouse and human
 RT receptors.";

RL Biochem. Biophys. Res. Commun. 193:356-363 (1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=CBA/CA;
 RX MEDLINE=93391374; PubMed=8378320;
 RA Cao X., Korak C.A., Liu Y.J., Noguchi M., O'Connell E., Leonard W.J.;
 RT "Characterization of cDNAs encoding the murine interleukin 2 receptor
 RT (IL-2R) gamma chain: chromosomal mapping and tissue specificity of
 RT IL-2R gamma chain expression.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:8464-8468 (1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93366191; PubMed=8359699;
 RA Kobayashi N., Nakagawa S., Minami Y., Taniguchi T., Kono T.;
 RT "Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor
 RT gamma.";
 RL Gene 130:303-304 (1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95104285; PubMed=7805729;
 RA Disanto J.P., Certain S., Wilson A., Macdonald H.R., Avner P.,
 RA Fischer A., de Saint Basile G.;
 RT "The murine interleukin-2 receptor gamma chain gene: organization,
 RT chromosomal localization and expression in the adult thymus.";
 RL Eur. J. Immunol. 24:3014-3018 (1994).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX STRAIN=B6 S;
 RX MEDLINE=96341745; PubMed=8750189;
 RA Chiu R.K., Droll A., Cooper D.L., Dougherty S.T., Dirks J.F.,
 RA Dougherty G.J.;
 RT "Molecular mechanisms regulating the hyaluronan binding activity of
 RT the adhesion protein CD44.";
 RL J. Neurooncol. 26:231-239 (1995).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX STRAIN=FVB/N; TISSUE=Salivary gland;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- FUNCTION: Common subunit for the receptors for a variety of
 CC interleukins.
 CC -1- SUBUNIT: The gamma chain is common to the IL2, IL4, IL7, IL21 and
 CC probably also the IL13 receptors.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors.
 CC -1- Subfamily 5.
 CC -1- SIMILARITY: Contains 1 fibronectin type III domain.
 CC -----
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CC CC EMBL; D13821; BAA02974.1; -
DR DR EMBL; U21795; AAG4279.1; -
DR DR EMBL; D13865; BAA02760.1; -
DR DR EMBL; L20048; AAB39286.1; -
DR DR EMBL; S75852; AAB32804.1; -
DR DR EMBL; S75844; AAB32904.1; JOINED.
DR DR EMBL; S75845; AAB32904.1; JOINED.
DR DR EMBL; S75847; AAB32904.1; JOINED.
DR DR EMBL; S75848; AAB32904.1; JOINED.
DR DR EMBL; S75849; AAB32904.1; JOINED.
DR DR EMBL; S75850; AAB32904.1; JOINED.
DR DR EMBL; S75851; AAB32904.1; JOINED.
DR DR EMBL; X75337; CAA53085.1; -
DR DR EMBL; BC014720; AAB14720.1; -
DR DR PIR; I49280; I49280.
DR DR HSP; P31785; I11M.
DR DR MGD; MGI:96551; I12g9.
DR DR InterPro; IPR002996; CRIA.
DR DR InterPro; IPR008957; FN III-like.
DR DR InterPro; IPR003961; FN III.
DR DR InterPro; IPR003531; Hemtopoptn_s_F1.
DR DR Pfam; PF00041; fn3; 1
DR DR SMART; SM00060; FN3; 1
DR DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; signal.
FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 369 CYTOKINE RECEPTOR COMMON GAMMA CHAIN.
FT DOMAIN 23 263 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 264 284 POTENTIAL.
FT DOMAIN 285 369 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 151 250 FIBRONECTIN TYPE-III.
FT DISULFID 62 72 POTENTIAL.
FT DIPEPTID 102 115 POTENTIAL.
FT CARBOHYD 71 71 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 96 96 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 369 AA; 42241 MW; CB2DSAB459077AC7 CRC64;

Query Match 66.3%; Score 853.5; DB 1; Length 369;
Best Local Similarity 67.2%; Pred. No. 2.7e-63;
Matches 156; Conservative 33; Mismatches 42; Indels 1; Gaps 1;

2y 2 NTTLTPNGEDTADFLTTMTDLSVSTPLPLPEVQCFVFNVEYMNCTWNSSEFPQPT 61
Db 24 SSKVLMSSANEDIKADLITLSTAPEHLISAPTLPLPEVQCFVFNVEYMNCTWNSSEFPQAT 83

62 NLTHYWKNSDNDKVKCSHYLPSSEITSGCQLOKKEIHLQYTFVVOLODPREPROAT 121
84 NLTHYRYKVDNNTFQCSHYLPSSEITSGCQLOKEDIQLQYTFVVOLODPORRAV 143

122 QMLKLQNLVTPAPENITLHKLSEQLSELENNRFL-NHCLHLVQYRTDWDHSWTQSV 180
Db 144 QKLNQNLVTPAPENITLNLSEQLSELEKRWKSHIKERCLQYLVYRNSRDSWIELV 203

181 DYRHKFSLPVGGKRYTFVRSPNPLCSAQHWSEWSPHGWNTSKEN 232
Db 204 NHEPRFSLPSVDELKRYTFVRSPNPNICGSSQWQSKVQFVHWGHTVEEN 255
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RESULT 5

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ID I132 HUMAN STANDARD; PRT; 380 AA.
AC Q14627; C00667;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Interleukin-13 receptor alpha-2 chain precursor (Interleukin-13
binding protein).
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GN IL13RA2 OR IL13R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Renal cell carcinoma;
RX MEDLINE=96279273; PubMed=8663118;
RA Caput D.; Laurent P.; Kaghad M.; Lelias J.M.; Lefort S.; Vita N.;
RA Ferrara P.;
RT "Cloning and characterization of a specific interleukin (IL)-13
RT binding protein structurally related to the IL-5 receptor alpha
RT chain.";
RL J. Biol. Chem. 271:16921-16926(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Donaldson D.D.; Whitters M.J.; Fitz L.; Neben T.; Finnerty H.;
RA Henderson S.L.; O'Hara R.M. Jr.; Turner K.J.; Wood C.R.; Collins M.;
RA Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97321053; PubMed=9177784;
RA Guo J.; Apiou F.; Mellerin M.P.; Lebeau B.; Jacques Y.; Minvielle S.;
RA "Chromosome mapping and expression of the human interleukin-13
RA receptor.";
RL Genomics 42:141-145(1997).
RN [4]
RP SEQUENCE FROM N.A.
RA Whitehead S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung, and Prostate;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg K.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;
RA Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;
RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;
RA Datchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;
RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;
RA Brownstein M.J.; Usdin T.B.; Toshiyuki S.; Carninci P.; Prange C.;
RA Raha S.S.; Loughran N.A.; Peters G.J.; Abramson R.D.; Mullen S.J.;
RA Bosak S.A.; McSwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;
RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;
RA Villalón D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;
RA Fahey J.; Helton E.; Kettman M.; Madan A.; Rodriguez S.; Sanchez A.;
RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;
RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;
RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.N.;
RA Butterfield Y.S.N.; Krzywinski M.I.; Skalska U.; Smal M.A.;
RA Schnerch A.; Schein J.E.; Jones S.J.M.; Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RL human and mouse cDNA sequences.";
CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Binds as a monomer with high affinity to interleukin 13
CC (IL13), but not to IL4.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC -!- SIMILARITY: Subfamily 5.
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
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CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL; X95302; CAA64617.1; -
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DR EMBL; U70981; AAB17170.1; -.
DR EMBL; Y08768; CAA70021.1; -.
DR EMBL; AL121878; CAD18962.1; -.
DR EMBL; BC020739; AAH20739.1; -.
DR EMBL; BC033705; AAH33705.1; -.
DR Genew; HGNC:5975; IL13RA2.
DR MIM; 300130; -.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005625; C:soluble fraction; TAS.
DR GO; GO:0004907; F:interleukin receptor activity; TAS.
DR GO; GO:0004871; F:signal transducer activity; TAS.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003532; Hemopoptn_S_F2.
DR Pfam; PF00441; fn3; 1.
DR PROSITE; PS01356; HEMATOPO REC_S_F2; 1.
DR Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 380
FT DOMAIN 27 343
FT TRANSMEM 344 363
FT DOMAIN 364 380
FT DISULFID 145 155
FT CARBOHYD 115 115
FT CARBOHYD 215 215
FT CARBOHYD 290 290
FT CARBOHYD 299 299
FT SEQUENCE 380 AA; 44176 MW; 3C6ACB1B5562C687 CRC64;
Query Match 16.1%; Score 207; DB 1; Length 380;
Best Local Similarity 25.4%; Pred. No. 6.1e-10;
Matches 60; Conservative 46; Mismatches 106; Indels 24; Gaps 9;
QY 9 NGNEDTADFFLTMTDLSLSTLPLRVCQVFVNVYVNCVWSSSEPOP-----T 61
DB 115 NGSE-VQSSAETTYWISQGPETKQVQDCVYVNWQYLLCSW-----RKGIVLDT 167
QY 62 NLTFLHYKNSNDKVKSHYLFSEITSGCQLOKKEIHLVYTFVQLQDPRE--PRQ 119
DB 168 NYNLFVYEGLDH--ALQCVDYIKADQNGICRFPYLEASDYKDFVCVSSSENKPIRS 225
QY 120 ATOMLKLQNLVPAENITLHKLSSQLELNNW---NRFNLHCHLEHLVQVETDWDHSWT 176
DB 226 SYTFQLQNLVPLPVPVYVYTFRESSEIKLWISPLGPIPARCFDYELREIKD--DTLLV 284
QY 177 EQSDVYRHKFLSPVDGQKRYTPFRVSRFNPLCGSAQHWSESHPIHW--GSNTSKE 231
DB 285 TATVE-NEITYLTKTTNTRQLCFVVSQVSKVNIYCSDDGIWSEWDKQWEGEDLSKK 339
RESULT 6
ID 1131 MOUSE STANDARD; PRT; 424 AA.
AC 009030;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-13RA-1) (Interleukin-13 binding protein) (NR4).
GN IL13RA1 OR IL13RA OR IL13R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=96133964; PubMed=8552669;
RX Hilton D.J., Zhang J.-G., Metcalf D., Alexander W.S., Nicola N.A.,
RA Willson T.A.;
RT "Cloning and characterization of a binding subunit of the interleukin 13 receptor that is also a component of the interleukin 4 receptor.";

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RL [2]
RN Proc. Natl. Acad. Sci. U.S.A. 93:497-501(1996).
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Brain, and Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datschenko L., Marusina A., Farmer A., Rubin G.M., Hong L.,
RA Sapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RC FUNCTION: Binds IL13 with a low affinity. Together with IL4R-alpha
can form a functional receptor for IL13. Also serves as an
alternate accessory protein to the common cytokine receptor gamma
chain for IL4 signaling, but cannot replace the function of gamma
C in allowing enhanced IL2 binding activity (By similarity).
CC -1- SUBUNIT: Interleukin 13 receptor is a complex of IL4R, IL13RA1,
and possibly other components (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Spleen, liver, thymus, heart, lung, kidney,
testis, stomach, brain, skin, and colon; but not skeletal muscle.
CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors.
Subfamily 5.
-----
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or send an email to license@isb-sib.ch).
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EMBL; S80963; AAB50695.1; -.
EMBL; BC052425; AAH52425.2; -.
EMBL; BC059339; AAH59339.1; -.
MGD; MGI:105052; Il13ral.
InterPro; IPR002996; CRIA.
InterPro; IPR008957; FN_III-like.
InterPro; IPR003961; FN_III.
InterPro; IPR003532; Hemopoptn_S_F2.
SMART; SM00600; FN3; 1.
PROSITE; PS01356; HEMATOPO REC_S_F2; 1.
Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 25
FT CHAIN 26 424
FT DOMAIN 26 340
FT TRANSMEM 341 364
FT DOMAIN 365 424
FT DISULFID 44 93
FT DISULFID 132 142
FT DISULFID 171 183
FT CARBOHYD 35 35
FT CARBOHYD 59 59
FT CARBOHYD 103 103
FT CARBOHYD 136 136
FT CARBOHYD 262 262
FT CARBOHYD 338 338
FT SEQUENCE 424 AA; 48402 MW; EB8330A0DC82C9F CRC64;

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Query Match 14.1%; Score 181.5; DB 1; Length 424;
Best Local Similarity 27.6%; Pred. No. 8.8e-08;
Matches 56; Conservative 38; Mismatches 86; Indels 23; Gaps 9;
CY 37 EVQCFFVNEVMCTWSSSPQ-P-TNLTLYWYKNSDNDKVKCSH-XLPSEITSGCQ 94
DB 129 ELKCIWNLNLSKSWLPGRTSDPTHTLYWY--SSLEKSKQCENYREGQHIACSPK 186
CY 95 LQKKEIHL-YQTFVVOLODPREPRQATQMLKQNLVWPAPENLTILKLSQLELNWN 153
DB 187 LTKVEPSFPHONQVMKDNAGKIRPSKIVSLTSYVKP-DPHIKHLLKNGALLVQWK 245
CY 154 N-REFLNHCLEHLVQY---RFD-----WDHSWTEQSDVDYRHKFLSPVQDQKRY 197
DB 246 NPQFRGRCLTYEVVNTQDRNILEVEDKQNSDRNMEGTSCFQLPGLVADAVY 305
CY 198 TFRVRSRFLPC-GSAQWSEWS 219
DB 306 TVRVKTNKLCFDDNKLWSDWS 328
RESULT 7
ID 1131_HUMAN STANDARD; PRT; 427 AA.
AC P78552; Q95646; Q95656;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-
DE 13RA-1) (CD213a1 antigen).
DE JN IL13RA1 OR IL13RA OR IL13R.
DS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Carcinoma;
RX MEDLINE=97165986; PubMed=9013879;
RA Miloux B., Laurent P., Bonnin O., Lupker J., Caput D., Vita N.,
RA Ferrara P.;
RT "Cloning of the human IL-13R alpha chain and reconstitution with the
RT IL-13R alpha of a functional IL-4/IL-13 receptor complex.";
RL FEBS Lett. 401:163-166 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Gauchat J.F.M., Schlagenhauf E., Feng N.P., Moser R., Yamage M.,
RA Jeannin P., Alouani S., Elson G., Notarangelo L.D., Wells T.,
RA Eugster H.P., Bonnefoy J.Y.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=97067184; PubMed=8910586;
RA Anan M.J., Tayebi N., Obiri N.I., Puri R.K., Modi W.S.,
RA Leonard W.J.;
RT "cDNA cloning and characterization of the human interleukin 13
RT receptor alpha chain.";
RL J. Biol. Chem. 271:29265-29270 (1996).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchwood J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Binds IL13 with a low affinity. Together with IL4R-alpha
CC can form a functional receptor for IL13. Also serves as an
CC alternate accessory protein to the common cytokine receptor gamma
CC chain for IL4 signaling, but cannot replace the function of gamma
CC C in allowing enhanced IL2 binding activity.
CC -!- SUBUNIT: Interleukin 13 receptor is a complex of IL4R, IL13RA1,
CC and possibly other components.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Ubiquitous. Highest levels in heart, liver,
CC skeletal muscle and ovary; lowest levels in brain, lung and
CC kidney. Also found in B-cells, T-cells and endothelial cells.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC Subfamily 5.
CC -!- DATABASE: NAME=PROW; NOTE=PROW 2:95-100(2001);
CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/435859885.g.htm".
CC -----
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CC -----
CC EMBL; Y10659; CAA71669.1; -;
CC EMBL; Y09328; CAA70508.1; -;
CC EMBL; U62858; AAB37127.1; -;
CC EMBL; U81379; AAD00510.3; -;
CC EMBL; BC009960; AAO09960.1; -;
CC Genew; HGNC:5974; IL13RA1.
CC MIM; 300119; -;
CC GO; GO:0005898; C:interleukin-13 receptor complex; TAS.
CC GO; GO:0005886; C:plasma membrane; TAS.
CC GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
CC InterPro; IPR002996; CR1A.
CC InterPro; IPR008957; FN III-like.
CC PROSITE; PS01356; HEMATOPOIETIN_F2; 1.
CC Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 427
FT DONAIN 22 343
FT TRANSMEM 344 367
FT DONAIN 368 427
FT DISULFID 46 95
FT DISULFID 134 144
FT DISULFID 173 185
FT CARBOHYD 37 37
FT CARBOHYD 61 61
FT CARBOHYD 105 105
FT CARBOHYD 138 138
FT CARBOHYD 157 157
FT CARBOHYD 235 235
FT CARBOHYD 265 265
FT CARBOHYD 293 293
FT CARBOHYD 329 329
FT CARBOHYD 341 341
FT CONFLICT 130 130
T -> I (IN REF. 3).
FT SIGNAL 1 21
FT CHAIN 22 427
FT DONAIN 22 343
FT TRANSMEM 344 367
FT DONAIN 368 427
FT DISULFID 46 95
FT DISULFID 134 144
FT DISULFID 173 185
FT CARBOHYD 37 37
FT CARBOHYD 61 61
FT CARBOHYD 105 105
FT CARBOHYD 138 138
FT CARBOHYD 157 157
FT CARBOHYD 235 235
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FT CARBOHYD 329 329
FT CARBOHYD 341 341
FT CONFLICT 130 130
T -> I (IN REF. 3).
FT SIGNAL 1 21
FT CHAIN 22 427
FT DONAIN 22 343
FT TRANSMEM 344 367
FT DONAIN 368 427
FT DISULFID 46 95
FT DISULFID 134 144
FT DISULFID 173 185
FT CARBOHYD 37 37
FT CARBOHYD 61 61
FT CARBOHYD 105 105
FT CARBOHYD 138 138
FT CARBOHYD 157 157
FT CARBOHYD 235 235
FT CARBOHYD 265 265
FT CARBOHYD 293 293
FT CARBOHYD 329 329
FT CARBOHYD 341 341
FT CONFLICT 130 130
T -> I (IN REF. 3).
FT SIGNAL 1 21
FT CHAIN 22 427
FT DONAIN 22 343
FT TRANSMEM 344 367
FT DONAIN 368 427
FT DISULFID 46 95
FT DISULFID 134 144
FT DISULFID 173 185
FT CARBOHYD 37 37
FT CARBOHYD 61 61
FT CARBOHYD 105 105
FT CARBOHYD 138 138
FT CARBOHYD 157 157
FT CARBOHYD 235 235
FT CARBOHYD 265 265
FT CARBOHYD 293 293
FT CARBOHYD 329 329
FT CARBOHYD 341 341
FT CONFLICT 130 130
T -> I (IN REF. 3).
FT SIGNAL 1 21
FT CHAIN 22 427
FT DONAIN 22 343
FT TRANSMEM 344 367
FT DONAIN 368 427
FT DISULFID 46 95
FT DISULFID 134 144
FT DISULFID 173 185
FT CARBOHYD 37 37
FT CARBOHYD 61 61
FT CARBOHYD 105 105
FT CARBOHYD 138 138
FT CARBOHYD 157 157
FT CARBOHYD 235 235
FT CARBOHYD 265 265
FT CARBOHYD 293 293
FT CARBOHYD 329 329
FT CARBOHYD 341 341
FT CONFLICT 130 130
T -> I (IN REF. 3).
FT SIGNAL 1 21
FT CHAIN 22 427
FT DONAIN 22 343
FT TRANSMEM 344 367
FT DONAIN 368 427
FT DISULFID 46 95
FT DISULFID 134 144
FT DISULFID 173 185
FT CARBOHYD 37 37
FT CARBOHYD 61 61
FT CARBOHYD 105 105
FT CARBOHYD 138 138
FT CARBOHYD 157 157
FT CARBOHYD 235 235
FT CARBOHYD 265 265
FT CARBOHYD 293 293
FT CARBOHYD 329 329
FT CARBOHYD 341 341
FT CONFLICT 130 130
T -> I (IN REF. 3).
FT SIGNAL 1 21
FT CHAIN 22 427
FT DONAIN 22 343
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Cell 104:291-300(2001).

[6]

VARIANT PAP THR-603.

MEDLINE=98058653; PubMed=9410898;

Dirksen U., Nishinakamura R., Gronck P., Hattenhorst U., Noguee L.,

Muray R., Burdach S.;

"Human pulmonary alveolar proteinosis associated with a defect in

GM-CSF/IL-3/IL-5 receptor common beta chain expression.";

J. Clin. Invest. 100:2211-2217(1997).

CC CC -|- FUNCTION: High affinity receptor for interleukin-3, interleukin-5

CC CC and granulocyte-macrophage colony-stimulating factor

CC CC -|- SUBUNIT: Heterodimer of an alpha and a beta chain. The beta chain

CC CC is common to the IL3, IL5 and GM-CSF receptors.

CC CC -|- SUBCELLULAR LOCATION: Type I membrane protein.

CC CC -|- DISEASE: Defects in CSF2RB are a cause of congenital pulmonary

CC CC alveolar proteinosis (PAP) [MTM:265120]. PAP is an autosomal

CC CC recessive fatal respiratory disease.

CC CC -|- SIMILARITY: Belongs to the type I cytokine family of receptors.

CC CC Subfamily 4.

CC CC -|- SIMILARITY: Contains 2 fibronectin type III domains.

CC CC -|- DATABASE: NAFS=PROW; NOPS=CD guide CDW131 entry;

CC CC WWW= <http://www.ncbi.nlm.nih.gov/prow/cd/cdw131.htm>.

CC CC -----

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CC CC or send an email to license@sib-sib.ch).

CC CC -----

EMBL; M59941; AAA18171.1; -;

DR DR PDB; 1C8P; 21-JUN-00.

DR DR PDB; 1EG2; 15-FEB-01.

DR DR PDB; 1GH7; 28-NOV-01.

DR DR Gene; HGNC:2436; CSF2RB.

DR DR MIM; 138981; -;

DR DR MIM; 265120; -;

DR DR GO; GO:0030526; C:granulocyte macrophage colony-stimulating f. . . ; TAS.

DR DR GO; GO:0004312; F:interleukin-3 receptor activity; TAS.

DR DR GO; GO:0004914; F:interleukin-5 receptor activity; TAS.

DR DR GO; GO:0004872; P:receptor activity; TAS.

DR DR GO; GO:0007585; P:respiratory gaseous exchange; TAS.

DR DR GO; GO:0007165; P:signal transduction; TAS.

DR DR InterPro; IPR002996; CR1A.

DR DR InterPro; IPR002822; Cytok_receptor_2.

DR DR InterPro; IPR008957; FN_III-like.

DR DR InterPro; IPR003961; FN_III.

DR DR InterPro; IPR003531; Hemtopoptn_S_F1.

DR DR Pfam; PF00041; fn3; 2.

DR DR SMART; SM00060; FN3; 2.

DR DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.

DR DR Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;

DR DR Disease mutation; 3D-structure.

DR DR SIGNAL 1 16 POTENTIAL.

DR DR CHAIN 17 897 CYTOKINE RECEPTOR COMMON BETA CHAIN.

DR DR DOMAIN 17 443 EXTRACELLULAR (POTENTIAL).

DR DR TRANSMEM 444 460 POTENTIAL.

DR DR DOMAIN 461 897 CYTOPLASMIC (POTENTIAL).

DR DR TRANSMEM 129 238 FIBRONECTIN TYPE-III 1.

DR DR DOMAIN 336 434 FIBRONECTIN TYPE-III 2.

DR DR DISULFID 35 45

DR DR DISULFID 75 96

DR DR DISULFID 86 91

DR DR DISULFID 250 260

DR DR DISULFID 289 306

DR DR CARBOHYD 58 58

DR DR CARBOHYD 191 191

DR DR CARBOHYD 346 346

DR DR VARIANT 603 603

DR DR VARIANT 647 647

DR DR VARIANT 647 647

DR DR N-LINKED (GLCNAC. . .)

DR DR N-LINKED (GLCNAC. . .)

DR DR N-LINKED (GLCNAC. . .) (POTENTIAL).

DR DR P -> T (in PAP; dbSNP:1801122)

DR DR FTTd=VAR_014801.

DR DR G -> V (in dbSNP:1801115).

DR DR FTTd=VAR_014802.

Db 185 VQTOCKINRLNAGMYVQVRCMLDP-----GKSEWS 217

RESULT 13

PRIR COLLI STANDARD; PRT; 830 AA.
AC Q90374;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Prolactin receptor precursor (PRL-R).
GN PRLR.
OS Columba livia (Domestic pigeon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
OX NCBI_TaxID=8932;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=CropSac;
RX MEDLINE=94283267; PubMed=7516866;
RA Chen X., Horseman N.D.;
RT "Cloning, expression, and mutational analysis of the pigeon prolactin receptor.";
RL Endocrinology 135:269-276(1994).
CC -!- FUNCTION: This is a receptor for the anterior pituitary hormone prolactin.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors. Subfamily 1.
CC -!- SIMILARITY: Contains 4 fibronectin type III domains.
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CC -----

EMBL; U07694; AAA20646.1; -

PIR; I50455; I50455.

HSSP; P16471; 1BP3.

InterPro; IPR002996; CRIA.

InterPro; IPR008957; FN III-like.

InterPro; IPR003961; FN III.

InterPro; IPR003528; Hemtopoptn_L_F1.

Pfam; PF00041; Fn3; 4.

SMART; SM00060; FN3; 4.

PROSITE; PS01352; HEMATOPO REC_L_F1; 1.

Receptor; Transmembrane; Glycoprotein; Signal; Repeat.

SIGNAL 1 23

CHAIN 24 830 PROLACTIN RECEPTOR.

DOMAIN 24 439 EXTRACELLULAR (POTENTIAL).

TRANSMEM 440 460 POTENTIAL.

DOMAIN 461 830 CYTOPLASMIC (POTENTIAL).

DOMAIN 25 122 FIBRONECTIN TYPE-III 1.

DOMAIN 123 226 FIBRONECTIN TYPE-III 2.

DOMAIN 229 326 FIBRONECTIN TYPE-III 3.

DOMAIN 327 429 FIBRONECTIN TYPE-III 4.

DISULFID 36 46 BY SIMILARITY.

DISULFID 75 86 BY SIMILARITY.

CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 304 304 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).

SEQUENCE 830 AA; 94507 MW; 38074E83CDF69E9F CRC64;

Query Match

10.3%; Score 132.5; DB 1; Length 830;

Best Local Similarity 22.2%; Pred. No. 0.0022;
Matches 44; Conservative 37; Mismatches 96; Indels 21; Gaps 7;
QY 38 VOCFVFNVEYMNCTWNSSE-PQPTNLTLHYWYKNSDNDKVQKCHYLFSBITSGCQLQ 96
DB 34 IRCRSLEKETFCWKPFGSDGGLPTNYTL--PYSKDSSEKIYECPDYMSG--PNSCYFD 89
QY 97 KKEIHLHYQTFVVLQDPPRPRQAT--QWLKLNLYVWPAPENLTILH---KLSEQLLEN 151
DB 90 KKHITPWTITNYITVMAMNEIGNSSDPQVVDVTISIVQDPAPVNLSTKTSTASTTYLLAK 149
QY 152 WNNRFL-----NHCLHLVQYRTDWDHSWTSQSYDYRHKFSLPSVDGQKRYTFVRSRF 205
DB 150 WSPPLADVTNSHVRYELRLKPEKEWETVSGVQTVQKVNRLQAGVKYVQVRCVL 209
QY 206 NPLCGSAQHWSEWSPHPIH 223
DB 210 D-----IGWSEWSSSRH 222

RESULT 14

IL4R MOUSE
ID IL4R MOUSE STANDARD; PRT; 810 AA.
AC P16382;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Interleukin-4 receptor alpha chain precursor (IL-4R-alpha).
GN IL4R OR IL4RA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.; SEQUENCE OF 26-39; 162-179 AND 194-210, AND ALTERNATIVE SPLICING
RX MEDLINE=90030408; PubMed=2805066;
RA Mosley B., Beckmann M.P., March C.J., Idzerda R.L., Gimpel S.D., Vanden Bos T., Friend D., Albert A., Anderson D., Jackson J., Wignall J.M., Smith C., Gallis B., Sims J.E., Urdal D., Widmer M.B., Cosman D., Park L.S.;
RA "The murine interleukin-4 receptor: molecular cloning and characterization of secreted and membrane bound forms.";
Cell 59:335-348(1989).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=90138976; PubMed=2405398;
RA Harada N., Castle B.E., Gorman D.M., Itoh N., Schreurs J., Barrett R.L., Howard M., Miyajima A.;
RA "Expression cloning of a cDNA encoding the murine interleukin 4 receptor based on ligand binding.";
Proc. Natl. Acad. Sci. U.S.A. 87:857-861(1990).
CC -!- FUNCTION: This is a receptor for interleukin-4. The soluble form of the IL4 receptor may represent a regulatory molecule specific for IL4-dependent immune responses.
CC -!- SUBUNIT: Heterodimer of an alpha chain and a common gamma chain.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein and secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=Membrane;
CC IsoId=P16382-1; Sequence=Displayed;
CC Note=Binds IL-4;
CC Name=2; Synonyms=Secreted;
CC IsoId=P16382-2; Sequence=VSP_001675, VSP_001676;
CC Note=Binds IL-4;
CC Name=3;
CC IsoId=P16382-3; Sequence=VSP_001677;
CC Note=Lacks the cytoplasmic domain. Binds IL-4;
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors. Subfamily 4.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation -

Db 412 YCARVRVK--PISNYDGIWSKWSSEYTW 437

Search completed: March 3, 2004, 12:36:12
Job time : 9.71896 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 3, 2004, 12:38:15 ; Search time 30.3268 Seconds
(without alignments)
1615.322 Million cell updates/sec

Title: US-09-825-561A-4

Perfect score: 1288

Sequence: 1 LNTTILPNGNEDTTADFFL.....QHWSEWHPHGSNTSKEN 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	1288	100.0	232	9	US-09-825-561A-4
2	1288	100.0	360	9	US-09-825-561A-18
3	1288	100.0	369	15	US-10-116-275-339
4	1288	100.0	691	9	US-09-935-868-20
5	1288	100.0	691	14	US-10-287-035-20
6	1288	100.0	691	14	US-10-282-162-20
7	1288	100.0	694	9	US-09-935-868-18
8	1288	100.0	694	9	US-09-935-868-22
9	1288	100.0	694	14	US-10-287-035-18
10	1288	100.0	694	14	US-10-287-035-22
11	1288	100.0	694	14	US-10-282-162-18
12	1288	100.0	694	14	US-10-282-162-22
13	1282	99.5	482	9	US-09-824-286-2
14	990.5	76.9	379	13	US-10-078-059-3
15	960	74.5	363	10	US-09-376-430-3

16	853.5	66.3	369	9	US-09-895-943-12	Sequence 12, Appl
17	853.5	66.3	369	9	US-09-895-593-12	Sequence 12, Appl
18	215	16.7	561	9	US-09-828-995B-72	Sequence 72, Appl
19	215	16.7	561	9	US-09-828-995B-81	Sequence 81, Appl
20	215	16.7	563	9	US-09-828-995B-78	Sequence 78, Appl
21	215	16.7	565	9	US-09-828-995B-75	Sequence 75, Appl
22	213	16.5	318	9	US-09-828-995B-69	Sequence 69, Appl
23	213	16.5	365	9	US-09-828-995B-66	Sequence 66, Appl
24	213	16.5	386	9	US-09-828-995B-61	Sequence 61, Appl
25	207	16.1	317	9	US-09-825-561A-84	Sequence 84, Appl
26	207	16.1	380	8	US-08-815-773-2	Sequence 2, Appl
27	207	16.1	380	9	US-09-871-617-2	Sequence 2, Appl
28	207	16.1	380	9	US-09-780-926-1	Sequence 1, Appl
29	207	16.1	380	10	US-09-090-867-2	Sequence 2, Appl
30	207	16.1	380	13	US-10-104-008-1	Sequence 1, Appl
31	206	16.0	255	9	US-09-828-995B-58	Sequence 58, Appl
32	203	15.8	380	8	US-08-815-773-4	Sequence 4, Appl
33	203	15.8	380	10	US-09-090-867-4	Sequence 4, Appl
34	183.5	14.2	372	8	US-08-815-773-7	Sequence 7, Appl
35	183.5	14.2	372	10	US-09-090-867-7	Sequence 7, Appl
36	181	14.1	776	14	US-10-287-035-36	Sequence 36, Appl
37	181	14.1	776	14	US-10-287-035-40	Sequence 40, Appl
38	181	14.1	776	14	US-10-287-035-44	Sequence 44, Appl
39	180	14.0	426	13	US-10-036-568-2	Sequence 2, Appl
40	179	13.9	778	9	US-09-935-868-46	Sequence 46, Appl
41	179	13.9	778	9	US-09-935-868-50	Sequence 50, Appl
42	179	13.9	778	14	US-10-287-035-46	Sequence 46, Appl
43	179	13.9	778	14	US-10-287-035-50	Sequence 50, Appl
44	179	13.9	778	14	US-10-287-035-56	Sequence 56, Appl
45	179	13.9	778	14	US-10-287-035-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1

US-09-825-561A-4
; Sequence 4, Application US/09825561A
; Patent No. US20020137677A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. US20020137677A1ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHALL CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; PRIOR FILING DATE: 2000-04-05
; PRIOR FILING DATE: 2000-04-05
; PRIOR FILING DATE: 2000-04-05
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-561A-4

Query Match	100.0%;	Score	1288;	DB	9;	Length	232;
Best Local Similarity	100.0%;	Pred. No.	1.3e+118;	Indels	0;	Gaps	0;
Matches	232;	Conservative	0;	Mismatches	0;		
QY	1	LNTTILPNGNEDTTADFFLTMTPTDSLSVSTPLPEVQCFFVFNVEYMNCTWNSSEPPQ	60				
DB	1	LNTTILPNGNEDTTADFFLTMTPTDSLSVSTPLPEVQCFFVFNVEYMNCTWNSSEPPQ	60				
QY	61	TNLTFLWYKNSNDKVKQCKSHYLFSEIITSGCLOKKEIHLTYCTFWOLODPRERQQA	120				
DB	61	TNLTFLWYKNSNDKVKQCKSHYLFSEIITSGCLOKKEIHLTYCTFWOLODPRERQQA	120				

QY 121 TQMLKQLNVLIPWAPENLTLLKLSQLELNNRFLNHLCHLHVQYRTDWDHWSWTEQSV 180
DB 121 TQMLKQLNVLIPWAPENLTLLKLSQLELNNRFLNHLCHLHVQYRTDWDHWSWTEQSV 180
QY 181 DYRHKFSPLPSVDGQKRYTFRVRSRFPNPLCGSAQHSWSESHPIHWSNTSKEN 232
DB 181 DYRHKFSPLPSVDGQKRYTFRVRSRFPNPLCGSAQHSWSESHPIHWSNTSKEN 232

RESULT 2

US-09-825-561a-18
; Sequence 18, Application US/09825561A
; Patent No. US20020137677A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHAL1 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: soluble human IL-2Rgamma/human kappa light chain
; OTHER INFORMATION: polypeptide
US-09-825-561a-18

Query Match 100.0%; Score 1288; DB 9; Length 360;
Best Local Similarity 100.0%; Pred. No. 2.3e-118;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNTTILTPNGNEDTTADFLTTMPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
DB 23 LNTTILTPNGNEDTTADFLTTMPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 82
QY 61 TNLTHYWKNSDNDKVKCSHYLFSSEITSGCOLKKEIHLVQYRTDWDHWSWTEQSV 120
DB 83 TNLTHYWKNSDNDKVKCSHYLFSSEITSGCOLKKEIHLVQYRTDWDHWSWTEQSV 142
QY 121 TQMLKQLNVLIPWAPENLTLLKLSQLELNNRFLNHLCHLHVQYRTDWDHWSWTEQSV 180
DB 143 TQMLKQLNVLIPWAPENLTLLKLSQLELNNRFLNHLCHLHVQYRTDWDHWSWTEQSV 202
QY 181 DYRHKFSPLPSVDGQKRYTFRVRSRFPNPLCGSAQHSWSESHPIHWSNTSKEN 232
DB 203 DYRHKFSPLPSVDGQKRYTFRVRSRFPNPLCGSAQHSWSESHPIHWSNTSKEN 254

RESULT 3

US-10-116-275-339
; Sequence 339, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and

; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 339
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Rat
; US-10-116-275-339

Query Match 100.0%; Score 1288; DB 15; Length 369;
Best Local Similarity 100.0%; Pred. No. 2.4e-118;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTILTPNGNEDTTADFLTTMPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
DB 23 LNTTILTPNGNEDTTADFLTTMPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 82
QY 61 TNLTHYWKNSDNDKVKCSHYLFSSEITSGCOLKKEIHLVQYRTDWDHWSWTEQSV 120
DB 83 TNLTHYWKNSDNDKVKCSHYLFSSEITSGCOLKKEIHLVQYRTDWDHWSWTEQSV 142
QY 121 TQMLKQLNVLIPWAPENLTLLKLSQLELNNRFLNHLCHLHVQYRTDWDHWSWTEQSV 180
DB 143 TQMLKQLNVLIPWAPENLTLLKLSQLELNNRFLNHLCHLHVQYRTDWDHWSWTEQSV 202
QY 181 DYRHKFSPLPSVDGQKRYTFRVRSRFPNPLCGSAQHSWSESHPIHWSNTSKEN 232
DB 203 DYRHKFSPLPSVDGQKRYTFRVRSRFPNPLCGSAQHSWSESHPIHWSNTSKEN 254

RESULT 4

US-09-935-868-20
; Sequence 20, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 691
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-20

Query Match 100.0%; Score 1288; DB 9; Length 691;
Best Local Similarity 100.0%; Pred. No. 5.4e-118;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTILTPNGNEDTTADFLTTMPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
DB 23 LNTTILTPNGNEDTTADFLTTMPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 82
QY 61 TNLTHYWKNSDNDKVKCSHYLFSSEITSGCOLKKEIHLVQYRTDWDHWSWTEQSV 120
DB 83 TNLTHYWKNSDNDKVKCSHYLFSSEITSGCOLKKEIHLVQYRTDWDHWSWTEQSV 142
QY 121 TQMLKQLNVLIPWAPENLTLLKLSQLELNNRFLNHLCHLHVQYRTDWDHWSWTEQSV 180
DB 143 TQMLKQLNVLIPWAPENLTLLKLSQLELNNRFLNHLCHLHVQYRTDWDHWSWTEQSV 202
QY 181 DYRHKFSPLPSVDGQKRYTFRVRSRFPNPLCGSAQHSWSESHPIHWSNTSKEN 232
DB 203 DYRHKFSPLPSVDGQKRYTFRVRSRFPNPLCGSAQHSWSESHPIHWSNTSKEN 254

RESULT 5

IS-10-287-035-20
Sequence 20, Application US/10287035
Publication No. US20030104567A1
GENERAL INFORMATION:
APPLICANT: Neil Stahl and George D. Yancopoulos
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
FILE REFERENCE: REG 203DA
CURRENT APPLICATION NUMBER: US/10/287,035
PRIOR FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: USSN 09/935,868
PRIOR FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: USSN 09/787,835
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: USSN 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 60
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 691
TYPE: PRT
ORGANISM: Homo sapiens
S-10-287-035-20

Query Match 100.0%; Score 1288; DB 14; Length 691;
Best Local Similarity 100.0%; Pred. No. 5.4e-118;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 1 LNTTLTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPOP 60
b 23 LNTTLTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPOP 82
Y 61 TNLTHWYKNSDNDKVQKSHYLFSEETSGCOLQKKEIHLVQYRTDWDHSWTEQSV 120
b 83 TNLTHWYKNSDNDKVQKSHYLFSEETSGCOLQKKEIHLVQYRTDWDHSWTEQSV 142
Y 121 TOMLKLQNLVWPAPENLTJLHKLSESOLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 180
b 143 TOMLKLQNLVWPAPENLTJLHKLSESOLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 202
Y 181 DYRHKFSLPVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSKEN 232
b 203 DYRHKFSLPVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSKEN 254

RESULT 6

S-10-282-162-20
Sequence 20, Application US/10282162
Publication No. US20030143697A1
GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
FILE REFERENCE: REG 203-B-US
CURRENT APPLICATION NUMBER: US/10/282,162
PRIOR FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 09/787,835
PRIOR FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 691
TYPE: PRT
ORGANISM: Homo sapiens
S-10-282-162-20

Query Match 100.0%; Score 1288; DB 14; Length 691;
Best Local Similarity 100.0%; Pred. No. 5.4e-118;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNTTLTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPOP 60
Db 23 LNTTLTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPOP 82
QY 61 TNLTHWYKNSDNDKVQKSHYLFSEETSGCOLQKKEIHLVQYRTDWDHSWTEQSV 120
Db 83 TNLTHWYKNSDNDKVQKSHYLFSEETSGCOLQKKEIHLVQYRTDWDHSWTEQSV 142
QY 121 TOMLKLQNLVWPAPENLTJLHKLSESOLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 180
Db 143 TOMLKLQNLVWPAPENLTJLHKLSESOLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 202
QY 181 DYRHKFSLPVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSKEN 232
Db 203 DYRHKFSLPVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSKEN 254

RESULT 7

US-09-935-868-18
Sequence 18, Application US/09935868
Patent No. US20020164690A1
GENERAL INFORMATION:
APPLICANT: Regeneron Pharmaceuticals, Inc.
TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
CURRENT APPLICATION NUMBER: US/09/935,868
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patent in version 3.0
SEQ ID NO 18
LENGTH: 694
TYPE: PRT
ORGANISM: Homo sapiens
US-09-935-868-18

Query Match 100.0%; Score 1288; DB 9; Length 694;
Best Local Similarity 100.0%; Pred. No. 5.5e-118;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNTTLTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPOP 60
Db 23 LNTTLTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPOP 82
QY 61 TNLTHWYKNSDNDKVQKSHYLFSEETSGCOLQKKEIHLVQYRTDWDHSWTEQSV 120
Db 83 TNLTHWYKNSDNDKVQKSHYLFSEETSGCOLQKKEIHLVQYRTDWDHSWTEQSV 142
QY 121 TOMLKLQNLVWPAPENLTJLHKLSESOLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 180
Db 143 TOMLKLQNLVWPAPENLTJLHKLSESOLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 202
QY 181 DYRHKFSLPVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSKEN 232
Db 203 DYRHKFSLPVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSKEN 254

RESULT 8

US-09-935-868-22
Sequence 22, Application US/09935868
Patent No. US20020164690A1
GENERAL INFORMATION:
APPLICANT: Regeneron Pharmaceuticals, Inc.
TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
FILE REFERENCE: REG 203D
CURRENT APPLICATION NUMBER: US/09/935,868
CURRENT FILING DATE: 2002-04-11

;; PRIOR APPLICATION NUMBER: PCT/US99/22045
;; PRIOR FILING DATE: 1999-09-22
;; NUMBER OF SEQ ID NOS: 52
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 22
;; LENGTH: 694
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-935-868-22

Query Match 100.0%; Score 1288; DB 9; Length 694;
Best Local Similarity 100.0%; Pred. No. 5.5e-118;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNTTLTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
DB 23 LNTTLTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 82
QY 61 TNLTHYWKNSDNDKVKCQSHYLFSEITSGCQLOKKEIHLVQTFVVOLODPREPRQA 120
DB 83 TNLTHYWKNSDNDKVKCQSHYLFSEITSGCQLOKKEIHLVQTFVVOLODPREPRQA 142
QY 121 TQMLKQLNVLIPWAPENLTLLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHSHWTEQSV 180
DB 143 TQMLKQLNVLIPWAPENLTLLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHSHWTEQSV 202
QY 181 DYRHKFSLPVSDGQKRYTFRVRSRFPNLCGSAQHWSEWSHPHIGSNTSKEN 232
DB 203 DYRHKFSLPVSDGQKRYTFRVRSRFPNLCGSAQHWSEWSHPHIGSNTSKEN 254

RESULT 9

US-10-287-035-18
;; Sequence 18, Application US/10287035
;; Publication No. US20030104567A1
;; GENERAL INFORMATION:
;; APPLICANT: Neil Stahl and George D. Yancopoulos
;; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
;; FILE REFERENCE: REG 203DA
;; CURRENT APPLICATION NUMBER: US/10/287,035
;; PRIOR APPLICATION NUMBER: USN 09/935,868
;; PRIOR FILING DATE: 2001-08-23
;; PRIOR APPLICATION NUMBER: USN 09/787,835
;; PRIOR FILING DATE: 2001-03-22
;; PRIOR APPLICATION NUMBER: USN 09/313,942
;; PRIOR FILING DATE: 1999-05-19
;; PRIOR APPLICATION NUMBER: 60/101,858
;; NUMBER OF SEQ ID NOS: 60
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 18
;; LENGTH: 694
;; TYPE: PRT
;; ORGANISM: Homo sapiens

US-10-287-035-18
Query Match 100.0%; Score 1288; DB 14; Length 694;
Best Local Similarity 100.0%; Pred. No. 5.5e-118;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTLTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
DB 23 LNTTLTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 82
QY 61 TNLTHYWKNSDNDKVKCQSHYLFSEITSGCQLOKKEIHLVQTFVVOLODPREPRQA 120
DB 83 TNLTHYWKNSDNDKVKCQSHYLFSEITSGCQLOKKEIHLVQTFVVOLODPREPRQA 142
QY 121 TQMLKQLNVLIPWAPENLTLLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHSHWTEQSV 180

DB 143 TQMLKQLNVLIPWAPENLTLLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHSHWTEQSV 202
QY 181 DYRHKFSLPVSDGQKRYTFRVRSRFPNLCGSAQHWSEWSHPHIGSNTSKEN 232
DB 203 DYRHKFSLPVSDGQKRYTFRVRSRFPNLCGSAQHWSEWSHPHIGSNTSKEN 254

RESULT 10

US-10-287-035-22
;; Sequence 22, Application US/10287035
;; Publication No. US20030104567A1
;; GENERAL INFORMATION:
;; APPLICANT: Neil Stahl and George D. Yancopoulos
;; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
;; FILE REFERENCE: REG 203DA
;; CURRENT APPLICATION NUMBER: US/10/287,035
;; PRIOR APPLICATION NUMBER: USN 09/935,868
;; PRIOR FILING DATE: 2001-08-23
;; PRIOR APPLICATION NUMBER: USN 09/787,835
;; PRIOR FILING DATE: 2001-03-22
;; PRIOR APPLICATION NUMBER: USN 09/313,942
;; PRIOR FILING DATE: 1999-05-19
;; PRIOR APPLICATION NUMBER: 60/101,858
;; NUMBER OF SEQ ID NOS: 60
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 22
;; LENGTH: 694
;; TYPE: PRT
;; ORGANISM: Homo sapiens

US-10-287-035-22
Query Match 100.0%; Score 1288; DB 14; Length 694;
Best Local Similarity 100.0%; Pred. No. 5.5e-118;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTLTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
DB 23 LNTTLTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 82
QY 61 TNLTHYWKNSDNDKVKCQSHYLFSEITSGCQLOKKEIHLVQTFVVOLODPREPRQA 120
DB 83 TNLTHYWKNSDNDKVKCQSHYLFSEITSGCQLOKKEIHLVQTFVVOLODPREPRQA 142
QY 121 TQMLKQLNVLIPWAPENLTLLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHSHWTEQSV 180
DB 143 TQMLKQLNVLIPWAPENLTLLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHSHWTEQSV 202
QY 181 DYRHKFSLPVSDGQKRYTFRVRSRFPNLCGSAQHWSEWSHPHIGSNTSKEN 232
DB 203 DYRHKFSLPVSDGQKRYTFRVRSRFPNLCGSAQHWSEWSHPHIGSNTSKEN 254

RESULT 11

US-10-282-162-18
;; Sequence 18, Application US/10282162
;; Publication No. US20030143697A1
;; GENERAL INFORMATION:
;; APPLICANT: REGENERON PHARMACEUTICALS, INC.
;; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
;; FILE REFERENCE: REG 203-B-US
;; CURRENT APPLICATION NUMBER: US/10/282,162
;; CURRENT FILING DATE: 2002-10-28
;; PRIOR APPLICATION NUMBER: 09/787,835
;; PRIOR FILING DATE: 1999-09-22
;; PRIOR APPLICATION NUMBER: PCT/US99/22045
;; PRIOR FILING DATE: 1999-09-22

US-10-282-162-18
Query Match 100.0%; Score 1288; DB 14; Length 694;
Best Local Similarity 100.0%; Pred. No. 5.5e-118;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNTTLTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
DB 23 LNTTLTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 82
QY 61 TNLTHYWKNSDNDKVKCQSHYLFSEITSGCQLOKKEIHLVQTFVVOLODPREPRQA 120
DB 83 TNLTHYWKNSDNDKVKCQSHYLFSEITSGCQLOKKEIHLVQTFVVOLODPREPRQA 142
QY 121 TQMLKQLNVLIPWAPENLTLLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHSHWTEQSV 180

NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-18

Query Match 100.0%; Score 1288; DB 14; Length 694;
Best Local Similarity 100.0%; Pred. No. 5.5e-118; Indels 0; Gaps 0;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y 1 LNTTILTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
Db 23 LNTTILTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 82
2y 61 TNLTLHYWYKNSDNDKVKCSHYLFSEITSGCOLQKKEIHLVQTFVVLQDPRPRQA 120
Db 83 TNLTLHYWYKNSDNDKVKCSHYLFSEITSGCOLQKKEIHLVQTFVVLQDPRPRQA 142
2y 121 TOMLKLQNLVTPWAPENLTLLKLSQLELNWNNRFLNHCLEHLVQRTDWDHSHWTEQSV 180
Db 143 TOMLKLQNLVTPWAPENLTLLKLSQLELNWNNRFLNHCLEHLVQRTDWDHSHWTEQSV 202
2y 181 DYRHKFLSPVDGQKRYTFRVRSRFPNPLCGSAQHSWSEWSPHIGWNTSKEN 232
Db 203 DYRHKFLSPVDGQKRYTFRVRSRFPNPLCGSAQHSWSEWSPHIGWNTSKEN 254

RESULT 12

US-10-282-162-22

; Sequence 22, Application US/10282162

; Publication No. US20030143697A1

; GENERAL INFORMATION:

; APPLICANT: REGENERON PHARMACEUTICALS, INC.

; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING

; FILE OF INVENTION: AND USING

; FILE REFERENCE: REG 203-B-US

; CURRENT APPLICATION NUMBER: US/10/282,162

; PRIOR FILING DATE: 2002-10-28

; PRIOR FILING DATE: 09/787,835

; PRIOR FILING DATE: 1999-09-22

; PRIOR FILING DATE: PCT/US99/22045

; NUMBER OF SEQ ID NOS: 56

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 22

; LENGTH: 694

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-282-162-22

Query Match 100.0%; Score 1288; DB 14; Length 694;
Best Local Similarity 100.0%; Pred. No. 5.5e-118; Indels 0; Gaps 0;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y 1 LNTTILTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
Db 23 LNTTILTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 82
2y 61 TNLTLHYWYKNSDNDKVKCSHYLFSEITSGCOLQKKEIHLVQTFVVLQDPRPRQA 120
Db 83 TNLTLHYWYKNSDNDKVKCSHYLFSEITSGCOLQKKEIHLVQTFVVLQDPRPRQA 142
2y 121 TOMLKLQNLVTPWAPENLTLLKLSQLELNWNNRFLNHCLEHLVQRTDWDHSHWTEQSV 180
Db 143 TOMLKLQNLVTPWAPENLTLLKLSQLELNWNNRFLNHCLEHLVQRTDWDHSHWTEQSV 202
2y 181 DYRHKFLSPVDGQKRYTFRVRSRFPNPLCGSAQHSWSEWSPHIGWNTSKEN 232
Db 203 DYRHKFLSPVDGQKRYTFRVRSRFPNPLCGSAQHSWSEWSPHIGWNTSKEN 254

RESULT 13

US-09-824-286-2

; Sequence 2, Application US/09824286

; Patent No. US20020028202A1

; GENERAL INFORMATION:

; APPLICANT: Burkly, Linda C

; Benjamin, Christopher D

; Hession, Catherine A

; Whitty, Adrian

; TITLE OF INVENTION: COMMON GAMMA CHAIN BLOCKING AGENTS

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Biogen, Inc.

; STREET: 14 Cambridge Center

; CITY: Cambridge

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02142

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/824,286

; FILING DATE: 02-Apr-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/017,466

; FILING DATE: 10-MAY-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Kaplan, Warren A.

; REGISTRATION NUMBER: 34,199

; REFERENCE/DOCKET NUMBER: A006 PCT CIP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617 679-2000

; TELEFAX: 617 679-2838

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 482 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: YES

; ANTI-SENSE: NO

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-824-286-2

Query Match 99.5%; Score 1282; DB 9; Length 482;
Best Local Similarity 99.6%; Pred. No. 1.3e-117;
Matches 231; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LNTTILTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 60
Db 23 LNTTILTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPPQ 82
Qy 61 TNLTLHYWYKNSDNDKVKCSHYLFSEITSGCOLQKKEIHLVQTFVVLQDPRPRQA 120
Db 83 TNLTLHYWYKNSDNDKVKCSHYLFSEITSGCOLQKKEIHLVQTFVVLQDPRPRQA 142
Qy 121 TOMLKLQNLVTPWAPENLTLLKLSQLELNWNNRFLNHCLEHLVQRTDWDHSHWTEQSV 180
Db 143 TOMLKLQNLVTPWAPENLTLLKLSQLELNWNNRFLNHCLEHLVQRTDWDHSHWTEQSV 202
Qy 181 DYRHKFLSPVDGQKRYTFRVRSRFPNPLCGSAQHSWSEWSPHIGWNTSKEN 232
Db 203 DYRHKFLSPVDGQKRYTFRVRSRFPNPLCGSAQHSWSEWSPHIGWNTSKEN 254

RESULT 14

US-10-078-059-3

; Sequence 3, Application US/10078059

Publication No. US20020193305A1

GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Cytokine Receptor Common Gamma Chain Like
FILE REFERENCE: PF466P2
CURRENT APPLICATION NUMBER: US/10/078,059
CURRENT FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: 60/269,876
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: PCT/US00/22493
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: 09/376,430
PRIOR FILING DATE: 1999-08-18
PRIOR APPLICATION NUMBER: 09/263,626
PRIOR FILING DATE: 1999-03-05
PRIOR APPLICATION NUMBER: PCT/US99/05068
PRIOR FILING DATE: 1999-03-05
PRIOR APPLICATION NUMBER: 60/086,505
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/078,563
PRIOR FILING DATE: 1998-03-19
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 379
TYPE: PRT
ORGANISM: Homo sapiens
US-10-078-059-3

Query Match 76.9%; Score 990.5; DB 13; Length 379;
Best Local Similarity 76.2%; Pred. No. 4.8e-89;
Matches 182; Conservative 21; Mismatches 29; Indels 7; Gaps 2;
QY 1 LNTTILTPNGNED-----TTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNS 54
DB 23 LNPKEFTPSGNEIDGKPGCTGGDFLTSTPAGTLDVSTLPLPKVQCFVFNVEYMNCTWNS 82
QY 55 SSEPQPTNLTHYWKYK-SDNDKVKQKSHYLFSEITSGCQLOKKEIHLTYTFVYVQLQDP 113
DB 83 SSEPQPTNLTHYGRNFGDDKLCQCHYLFSEITSGCWFGEIRLYTFVYVQLQDP 142
QY 114 REPRQATQMLKQLNVLIPWAPENITLHKLSQLELNWNNRFLNHCLEHLVQYRTDWDH 173
DB 143 REHRQPKQMLKQLDLVTPWAPENITLRLNLSFQLELSWSNRYLDHCLHLVQYRSRDR 202
QY 174 SWTEQSDYRHKFSPLPSVDGQKRYTFVRSRFNPPLCGSAQHSWSESHPIHWSNTSKEN 232
DB 203 SWTEQSDVHRHSFSLPSVDAQKLYTFVRSRYNPLCGSAQHSWSDWSYPIHWSNTSKEN 261

RESULT 15

US-09-376-430-3
Sequence 3, Application US/09376430
Publication No. US20030028006A1
GENERAL INFORMATION:
APPLICANT: Moore, Paul A.
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Cytokine Receptor Common Gamma Chain Like
FILE REFERENCE: PF466P1
CURRENT APPLICATION NUMBER: US/09/376,430
CURRENT FILING DATE: 1999-08-18
EARLIER APPLICATION NUMBER: 60/086,505
EARLIER FILING DATE: 1998-05-22
EARLIER APPLICATION NUMBER: 60/078,563
EARLIER FILING DATE: 1998-03-19
EARLIER APPLICATION NUMBER: 09/263,626
EARLIER FILING DATE: 1999-03-05
EARLIER APPLICATION NUMBER: PCT/US99/05068
EARLIER FILING DATE: 1999-03-05
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3

LENGTH: 363
TYPE: PRT
ORGANISM: Homo sapiens
US-09-376-430-3

Query Match 74.5%; Score 960; DB 10; Length 363;
Best Local Similarity 76.0%; Pred. No. 4.6e-86;
Matches 177; Conservative 20; Mismatches 32; Indels 4; Gaps 2;
QY 1 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEBPQ 60
DB 16 LNEDI---GKPGCTGGDFLTSTPAGTLDVSTLPLPKVQCFVFNVEYMNCTWNSSEBPQ 72
QY 61 TNLTHYWKYK-SDNDKVKQKSHYLFSEITSGCQLOKKEIHLTYTFVYVQLQDPREPRQ 119
DB 73 NNLTHYGRNFGDDKLCQCHYLFSEITSGCWFGEIRLYTFVYVQLQDPREHRQ 132
QY 120 ATOMLKLQNLVTPWAPENITLHKLSQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQS 179
DB 133 PQMLKQLDLVTPWAPENITLRLNLSFQLELSWSNRYLDHCLHLVQYRSRDRSRTQS 192
QY 180 VDYRHKFSPLPSVDGQKRYTFVRSRFNPPLCGSAQHSWSESHPIHWSNTSKEN 232
DB 193 VDRHSFSLPSVDAQKLYTFVRSRYNPLCGSAQHSWSDWSYPIHWSNTSKEN 245

Search completed: March 3, 2004, 12:50:51
Job time : 31.3268 secs

GenCore version 5.1.6
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3M protein - protein search, using sw model

run on: March 3, 2004, 12:31:49 ; Search time 15,5425 Seconds

(without alignments)
1435.834 Million cell updates/sec

Title: US-09-825-561A-4

Perfect score: 1288

Sequence: 1 LNTLTTPNGNEDTTADFFL.....QHWSEWSHPIHGSNTSKEN 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1288	100.0	369	2 A42565	interleukin-2 rece
2	1097	85.2	373	2 A55718	interleukin-2 rece
3	853.5	66.3	369	2 I49280	interleukin-2 rece
4	427.5	33.2	348	2 JC7807	common cytokine re
5	168.5	13.1	426	2 JC7773	IL-13Ralpha 1 prot
6	159	12.3	897	1 A39255	cytokine receptor
7	150	11.6	831	2 J01655	prolactin receptor
8	146.5	11.4	400	2 S06945	granulocyte-macrop
9	145.5	11.3	333	2 SI3884	granulocyte-macrop
10	136.5	10.6	896	2 I56563	interleukin-3 rece
11	135.5	10.5	378	2 S50040	granulocyte-macrop
12	132.5	10.3	830	2 I50455	prolactin receptor
13	132	10.2	810	1 A33380	interleukin-4 rece
14	125	9.7	896	1 A35782	cytokine receptor
15	121.5	9.4	581	2 I45971	prolactin receptor
16	119.5	9.3	800	1 S31575	interleukin-4 rece
17	118	9.2	415	2 SI2357	interleukin-5 rece
18	116	9.0	878	1 A40091	interleukin-3 rece
19	114	8.9	440	2 JLO144	interleukin-6 rece
20	114	8.9	460	2 JLO145	interleukin-6 rece
21	113	8.8	420	2 S21052	interleukin-5 rece
22	112	8.7	918	2 A36337	membrane glycoprot
23	110.5	8.6	359	2 JC7280	cytokine receptor-
24	110.5	8.6	551	2 A30342	interleukin-2 rece
25	109.5	8.5	292	2 I77525	prolactin receptor
26	109.5	8.5	303	2 I77524	prolactin receptor
27	109.5	8.5	608	2 I53269	prolactin receptor
28	108.5	8.4	310	2 A29884	prolactin receptor
29	108.5	8.4	412	2 A41070	prolactin receptor

30 108.5 8.4 610 2 A34631 lactogen receptor
31 108.5 8.4 610 2 A36116 prolactin receptor
32 107 8.3 335 2 A40267 interleukin-5 rece
33 105 8.2 539 2 A35052 interleukin-2 rece
34 104.5 8.1 286 2 S50039 granulocyte-macrop
35 104.5 8.1 917 2 I49699 glycoprotein 130 -
36 98.5 7.6 918 2 A44257 interleukin-6 sign
37 97.5 7.6 608 2 S32823 somatotropin recep
38 97.5 7.6 825 1 A60386 interleukin-4 rece
39 96.5 7.5 625 2 S35317 hemopoietic grow
40 96.5 7.5 626 2 S37622 proto-oncogene - m
41 95.5 7.4 288 2 B59405 prolactin receptor
42 95.5 7.4 376 2 A59405 prolactin receptor
43 95.5 7.4 622 2 A40144 prolactin receptor
44 95.5 7.4 630 2 I51086 prolactin receptor
45 94.5 7.3 26926 1 I38344 titin, cardiac mus

ALIGNMENTS

RESULT 1

A42565
interleukin-2 receptor gamma chain - human
C:Species: Homo sapiens (man)
C:Date: 04-Mar-1993 #sequence revision 18-Nov-1994 #text_change 17-Mar-2003
C:Accession: A42565; A46591; I54332
R:Takeishi, T.; Asao, H.; Ohtani, K.; Ishii, N.; Kumaki, S.; Tanaka, N.; Munakata, H.;
Science 257, 379-382, 1992
A>Title: Cloning of the gamma chain of the human IL-2 receptor.
A:Reference number: A42565; MUID:92335883; PMID:1631559
A:Accession: A42565
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid; protein
A:Residues: 1-369 <TA>
A:Cross-references: NID:G303611; PIDN:BAA01857.1; PID:G219890
A:Experimental source: MOLT beta lymphoid cells
A>Note: sequence extracted from NCBI Backbone (NCBIP:109167)
R:Noguchi, M.; Adelstein, S.; Cao, X.; Leonard, W.J.
J. Biol. Chem. 268, 13601-13608, 1993
A>Title: Characterization of the human interleukin-2 receptor gamma chain gene.
A:Reference number: A46591; MUID:93293887; PMID:8514792
A:Accession: A46591
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <RS>
A:Cross-references: GB:L12183; NID:G307056; PIDN:AAA59145.1; PID:G307058
R:Puck, J.M.; Deschenes, S.M.; Porter, J.C.; Dutra, A.S.; Brown, C.J.; Willard, H.F.; He
Hum. Mol. Genet. 2, 1099-1104, 1993
A>Title: The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated in X-link
A:Reference number: I54332; MUID:94004847; PMID:8401490
A:Accession: I54332
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <RE2>
A:Cross-references: GB:L19546; NID:G349631; PIDN:AAC37524.1; PID:G349632
C:Genetics:
A:Gene: GDB:IL2RG; SCIDX1: IMD4
A:Cross-references: GDB:I34807; OMIM:308380
A:Map position: Xq13.1-Xq13.1
A:Introns: 39/1; 90/2; 152/1; 198/3; 253/1; 285/2; 308/3
A>Note: defects are associated with an X-linked form of severe combined immunodeficiency
C:Superfamily: interleukin-2 receptor gamma chain
C:Keywords: cytokine receptor; duplication; immunodeficiency; transmembrane protein

Query Match 100.0%; Score 1288; DB 2; Length 369;

Best Local Similarity 100.0%; Pred. No. 7.7e-100; Indels 0; Gaps 0;
Matches 232; Conservative 0; Mismatches 0;

QY 1 LNTLTTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFFVFNVMNCTWNSSEPPQ 60

Db 23 LNTLTTPNGNEDTTADFFLTMTDLSVSTLPLPEVQCFFVFNVMNCTWNSSEPPQ 82

QY 61 TNLTLHYWYKNSDNDKVKQCSHYLSEETISGCOLQKEIHLVQYFVVLQDPPREPRQA 120
 Db 83 TNLTLHYWYKNSDNDKVKQCSHYLSEETISGCOLQKEIHLVQYFVVLQDPPREPRQA 142
 QY 121 TQMLKQLNLVWPAPENLTHKLSSEQLNWNRFNLHCLHLEHLVQYRTDWDHWSWTEQSV 180
 Db 143 TQMLKQLNLVWPAPENLTHKLSSEQLNWNRFNLHCLHLEHLVQYRTDWDHWSWTEQSV 202
 QY 181 DYRHKFSPLSDGQKRYTFRVRSRNPFLCGSAQHSWSESHPIHWSNTSKEN 232
 Db 203 DYRHKFSPLSDGQKRYTFRVRSRNPFLCGSAQHSWSESHPIHWSNTSKEN 254
 RESULT 2
 A55718
 interleukin-2 receptor gamma chain precursor - dog
 C:Species: Canis lupus familiaris (dog)
 C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 23-Jul-1999
 C:Accession: A55718
 R:Henthorn, P.S.; Somberg, R.L.; Fimiani, V.M.; Puck, J.M.; Patterson, D.F.; Felsburg, F.
 Genomics 23, 69-74, 1994
 A>Title: IL-2Rgamma Gene microdeletion demonstrates that canine X-linked severe combined
 A:Reference number: A55718; MUID:95130114; PMID:7829104
 A:Accession: A55718
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-373 <HEN>
 A:CROSS-references: GB:U04361; NID:9517411; PIDN:AA048403.1; PID:9517412
 C:Superfamily: interleukin-2 receptor gamma chain
 C:Keywords: cytokine receptor; duplication
 Query Match 85.2%; Score 1097; DB 2; Length 373;
 Best Local Similarity 82.8%; Pred. No. 6.4e-84;
 Matches 192; Conservative 24; Mismatches 16; Indels 0; Gaps 0;
 QY 1 LNTTLTPNGNEDTTADPFLTTMPTDSLSVSTLPPEVQCFVFNVEYVNCVTWNGSSSEPOP 60
 Db 23 LNSTVPMNGNEDITDPFLATPBTETLSVSLPLPEVQCFVFNVEYVNCVTWNGSSSEPRP 82
 QY 61 TNLTLHYWYKNSDNDKVKQCSHYLSEETISGCOLQKEIHLVQYFVVLQDPPREPRQA 120
 Db 83 TNLTLHYWYKNSDNDKVKQCSHYLSEETISGCOLQKEIHLVQYFVVLQDPPREPRQA 142
 QY 121 TQMLKQLNLVWPAPENLTHKLSSEQLNWNRFNLHCLHLEHLVQYRTDWDHWSWTEQSV 180
 Db 143 TQMLKQLNLVWPAPENLTHKLSSEQLNWNRFNLHCLHLEHLVQYRTDWDHWSWTEQSV 202
 QY 181 DYRHKFSPLSDGQKRYTFRVRSRNPFLCGSAQHSWSESHPIHWSNTSKEN 232
 Db 203 DHRNFSPLSDGQKRYTFRVRSRNPFLCGSAQHSWSESHPIHWSNTSKEN 254
 RESULT 3
 I49280
 interleukin-2 receptor gamma chain precursor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 20-Jun-2000
 C:Accession: I49280; A47514; JN0592; JN0775; S37582; I53398
 R:Cao, X.; Kozak, C.A.; Liu, Y.
 Proc. Natl. Acad. Sci. U.S.A. 90, 8464-8468, 1993
 A>Title: Characterization of cDNAs encoding the murine interleukin 2 receptor (IL-2R) g
 A:Reference number: A47514; MUID:93391374; PMID:8378320
 A:Accession: I49280
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-369 <CAO>
 A:CROSS-references: EMBL:U21795; NID:9727349; PIDN:AAA64279.1; PID:9727350
 A:Accession: A47514
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-369 <RE2>
 A:CROSS-references: GB:L20048; NID:9404067; PIDN:AAA39286.1; PID:9404068
 R:Kumaki, S.; Kondo, M.; Takeshita, T.; Asao, H.; Nakamura, M.; Sugamura, K.

Biochem. Biophys. Res. Commun. 193, 356-363, 1993
 A>Title: Cloning of the mouse interleukin 2 receptor gamma chain: Demonstration of func
 A:Reference number: JN0592; MUID:93277575; PMID:8503926
 A:Accession: JN0592
 A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-369 <KUM>
 A:CROSS-references: DDBJ:D13565; NID:9303684; PIDN:BA02760.1; PID:9303685
 R:Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T.
 Gene 130, 303-304, 1993
 A>Title: Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor gamma.
 A:Reference number: JN0775; MUID:93366191; PMID:8359699
 A:Accession: JN0775
 A:Molecule type: mRNA
 A:Residues: 1-369 <KOB>
 A:CROSS-references: GB:D13821; NID:9436045; PIDN:BA02974.1; PID:9436046
 R:Chiu, R.K.; Dougherty, G.J.
 submitted to the EMBL Data Library, October 1993
 A>Description: Regulation of CD44-mediated cellular adhesion by the IL-2 R gamma chain.
 A:Reference number: S37582
 A:Accession: S37582
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-350, 'S', 352-366, 'S', 368-369 <CHI>
 A:CROSS-references: EMBL:X75337
 R:Disanto, J.P.; Certain, S.; Wilson, A.; MacDonald, H.R.; Avner, P.; Fischer, A.; de S
 Eur. J. Immunol. 24, 3014-3018, 1994
 A>Title: The murine interleukin-2 receptor gamma chain gene: organization, chromosomal
 A:Reference number: I53398; MUID:95104285; PMID:7805729
 A:Accession: I53398
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-369 <RES>
 A:CROSS-references: GB:S75852; NID:9861554; PIDN:AAB32904.1; PID:9861555
 C:Genetics:
 A:Gene: IL-2Rgamma
 A:Introns: 39/1; 90/2; 152/1; 199/3; 254/1; 286/2; 308/3
 C:Complex: The high affinity receptor is a heterotrimer of alpha (see PIR:UHS2), beta
 eptors.
 C:Function:
 A>Description: receptor for interleukin-2
 A:Pathway: interleukin-2 stimulated growth and differentiation of T cells, B cells, NK
 C:Superfamily: interleukin-2 receptor gamma chain
 C:Keywords: cytokine receptor; duplication; glycoprotein; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-369/Product: interleukin-2 receptor gamma chain #status predicted <MAT>
 F:256-284/Domain: transmembrane #status predicted <TM>
 F:71,75,84,96,159,164,306/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 66.3%; Score 853.5; DB 2; Length 369;
 Best Local Similarity 67.2%; Pred. No. 1.2e-63;
 Matches 156; Conservative 33; Mismatches 42; Indels 1; Gaps 1;
 QY 2 NNTLTTPNGNEDTTADPFLTTMPTDSLSVSTLPPEVQCFVFNVEYVNCVTWNGSSSEPOP 61
 Db 24 SSKVLMSANEDIKADLIITSTAPHELAPTLPPEVQCFVFNVEYVNCVTWNGSSSEPOP 83
 QY 62 NLTLHYWYKNSDNDKVKQCSHYLSEETISGCOLQKEIHLVQYFVVLQDPPREPRQA 121
 Db 84 NLTLHYWYKNSDNDKVKQCSHYLSEETISGCOLQKEIHLVQYFVVLQDPPREPRQA 143
 QY 122 QMLKQLNLVWPAPENLTHKLSSEQLNWNRFNLHCLHLEHLVQYRTDWDHWSWTEQSV 180
 Db 144 QMLKQLNLVWPAPENLTHKLSSEQLNWNRFNLHCLHLEHLVQYRTDWDHWSWTEQSV 203
 QY 181 DYRHKFSPLSDGQKRYTFRVRSRNPFLCGSAQHSWSESHPIHWSNTSKEN 232
 Db 204 NHEPFSPLSDGQKRYTFRVRSRNPFLCGSAQHSWSESHPIHWSNTSKEN 255
 RESULT 4
 JC7907
 common cytokine receptor gamma chain, isoform a - chicken

C:\Species: Gallus gallus (chicken)
C:\Date: 03-Feb-2003 #sequence_revision 03-Feb-2003 #text_change 31-Mar-2003
C:\Accession: JC7907
R:\Min, W.; Lillehoj, H.S.; Fetterer, R.H.
Biochem. Biophys. Res. Commun. 299, 321-327, 2002
A:\Title: Identification of an alternatively spliced isoform of the common cytokine receptor
A:\Reference number: JC7907; MUID:23225486; PMID:12437989
A:\Accession: JC7907
A:\Molecule type: mRNA
A:\Residues: 1-348 <MIN>
A:\Cross-references: GB:AJ419897; GB:AJ419898
A:\Experimental source: egg
A:\Comment: This protein, expressed as a transmembrane glycoprotein, is a novel member of
A:\Genetics: 2; Genes: 1
A:\Gene: ch gamma-c-a

Query Match 33.2%; Score 427.5; DB 2; Length 348;
Best Local Similarity 42.9%; Pred. No. 3.5e-28;
Matches 91; Conservative 36; Mismatches 56; Indels 29; Gaps 9;

2Y 34 PLPE-VQCFVFNVMNCTWSSSPQPTNLTLYWYKNSDNDKVKQCSHYLSERITSG 92
DB 24 PSFGVECLIFEEYMTCTW-GSGQTLTANSLYLYWYEN--KLPVVCQOYLWDRSVRIG 80
2Y 93 COLQKEIHLVQTFVVO-----LQDPREPRQATQMLKQNLVWPAPENLTLLHL 143
DB 81 CFPESEIIQFAFVRVNASCGQTEIP-----SNRMELQNLVWPAPVNLTHNM 133
2Y 144 SSQLELNNRRF-LNHCLHLVQYRTDWDHSWTEQSDVYRHK---PSLSPVDGQKRYTF 199
DB 134 SQNLQTLTWSSPYKPEQCLHVVYKSKNDTSWTNOEV---XGVIFSPFSDVYKYYTF 189
2Y 200 VYRSFNPFCGSAQHSWSPHPHWGNS-TSK 230
DB 190 YYRSKINNYCGNTQLMSEWSPVFWGNNSTSK 221

RESULT 5
JC7773
IL-13ralpha 1 protein - rat
C:\Species: Rattus norvegicus (Norway rat)
C:\Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:\Accession: JC7773
R:\Pierrot, C.; Beniguel, L.; Beque, A.; Khalife, J.
Biochem. Biophys. Res. Commun. 287, 969-976, 2001
A:\Title: Expression of a functional IL-13ralpha by rat B cells.
A:\Reference number: JC7773; PMID:11573960
A:\Accession: JC7773
A:\Molecule type: mRNA
A:\Residues: 1-426 <PIE>
A:\Cross-references: GB:AY044251
A:\Comment: This protein is an functionally binding protein involved in B cell proliferation
A:\Genetics: 2; Genes: 1
A:\Gene: il-13ralpha

Query Match 13.1%; Score 168.5; DB 2; Length 426;
Best Local Similarity 25.5%; Pred. No. 1.7e-06;
Matches 54; Conservative 30; Mismatches 101; Indels 27; Gaps 8;

2Y 37 EQVCFVFNVMNCTWSSSPQPTNLTLYWYKNSDNDKVKQCSHYLSERITSGCQL 95
DB 129 ELQCTWNLSTYKCSWLPKQNTSPDNTLTLYWY--SSLGKSLQCEH-IHQCHIGCSF 185
2Y 96 QKKEI---HLVQTFVVOQDPREPRQATQMLKQNLVWPAPENLTLLHLKLSQLELAW 152
DB 186 KLTKVESYNEHHNIQIMWKDAGKIRPSYKIVTSNPKPGPHIKLF-LKNGALFVQW 244
2Y 153 NN--RFLNHCLHLVQYRTDWDHSWTEQSDVYRHK-----FSLSPVDGQ 194
DB 245 KNPQFSSRCUSYEVEVNSTQDTSNLSLEVBEDKQCNSEFDRNMEGASCFISPGVLXN 304
195 KRYTFVRSRFPNLC-GSAQHSWSPHPHWG 225

C:\Species: Gallus gallus (chicken)
C:\Date: 03-Feb-2003 #sequence_revision 03-Feb-2003 #text_change 31-Mar-2003
C:\Accession: JC7907
R:\Min, W.; Lillehoj, H.S.; Fetterer, R.H.
Biochem. Biophys. Res. Commun. 299, 321-327, 2002
A:\Title: Identification of an alternatively spliced isoform of the common cytokine receptor
A:\Reference number: JC7907; MUID:23225486; PMID:12437989
A:\Accession: JC7907
A:\Molecule type: mRNA
A:\Residues: 1-348 <MIN>
A:\Cross-references: GB:AJ419897; GB:AJ419898
A:\Experimental source: egg
A:\Comment: This protein, expressed as a transmembrane glycoprotein, is a novel member of
A:\Genetics: 2; Genes: 1
A:\Gene: ch gamma-c-a

Query Match 33.2%; Score 427.5; DB 2; Length 348;
Best Local Similarity 42.9%; Pred. No. 3.5e-28;
Matches 91; Conservative 36; Mismatches 56; Indels 29; Gaps 9;

2Y 34 PLPE-VQCFVFNVMNCTWSSSPQPTNLTLYWYKNSDNDKVKQCSHYLSERITSG 92
DB 24 PSFGVECLIFEEYMTCTW-GSGQTLTANSLYLYWYEN--KLPVVCQOYLWDRSVRIG 80
2Y 93 COLQKEIHLVQTFVVO-----LQDPREPRQATQMLKQNLVWPAPENLTLLHL 143
DB 81 CFPESEIIQFAFVRVNASCGQTEIP-----SNRMELQNLVWPAPVNLTHNM 133
2Y 144 SSQLELNNRRF-LNHCLHLVQYRTDWDHSWTEQSDVYRHK---PSLSPVDGQKRYTF 199
DB 134 SQNLQTLTWSSPYKPEQCLHVVYKSKNDTSWTNOEV---XGVIFSPFSDVYKYYTF 189
2Y 200 VYRSFNPFCGSAQHSWSPHPHWGNS-TSK 230
DB 190 YYRSKINNYCGNTQLMSEWSPVFWGNNSTSK 221

RESULT 5
JC7773
IL-13ralpha 1 protein - rat
C:\Species: Rattus norvegicus (Norway rat)
C:\Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:\Accession: JC7773
R:\Pierrot, C.; Beniguel, L.; Beque, A.; Khalife, J.
Biochem. Biophys. Res. Commun. 287, 969-976, 2001
A:\Title: Expression of a functional IL-13ralpha by rat B cells.
A:\Reference number: JC7773; PMID:11573960
A:\Accession: JC7773
A:\Molecule type: mRNA
A:\Residues: 1-426 <PIE>
A:\Cross-references: GB:AY044251
A:\Comment: This protein is an functionally binding protein involved in B cell proliferation
A:\Genetics: 2; Genes: 1
A:\Gene: il-13ralpha

Query Match 13.1%; Score 168.5; DB 2; Length 426;
Best Local Similarity 25.5%; Pred. No. 1.7e-06;
Matches 54; Conservative 30; Mismatches 101; Indels 27; Gaps 8;

2Y 37 EQVCFVFNVMNCTWSSSPQPTNLTLYWYKNSDNDKVKQCSHYLSERITSGCQL 95
DB 129 ELQCTWNLSTYKCSWLPKQNTSPDNTLTLYWY--SSLGKSLQCEH-IHQCHIGCSF 185
2Y 96 QKKEI---HLVQTFVVOQDPREPRQATQMLKQNLVWPAPENLTLLHLKLSQLELAW 152
DB 186 KLTKVESYNEHHNIQIMWKDAGKIRPSYKIVTSNPKPGPHIKLF-LKNGALFVQW 244
2Y 153 NN--RFLNHCLHLVQYRTDWDHSWTEQSDVYRHK-----FSLSPVDGQ 194
DB 245 KNPQFSSRCUSYEVEVNSTQDTSNLSLEVBEDKQCNSEFDRNMEGASCFISPGVLXN 304
195 KRYTFVRSRFPNLC-GSAQHSWSPHPHWG 225

C:\Species: Gallus gallus (chicken)
C:\Date: 03-Feb-2003 #sequence_revision 03-Feb-2003 #text_change 31-Mar-2003
C:\Accession: JC7907
R:\Min, W.; Lillehoj, H.S.; Fetterer, R.H.
Biochem. Biophys. Res. Commun. 299, 321-327, 2002
A:\Title: Identification of an alternatively spliced isoform of the common cytokine receptor
A:\Reference number: JC7907; MUID:23225486; PMID:12437989
A:\Accession: JC7907
A:\Molecule type: mRNA
A:\Residues: 1-348 <MIN>
A:\Cross-references: GB:AJ419897; GB:AJ419898
A:\Experimental source: egg
A:\Comment: This protein, expressed as a transmembrane glycoprotein, is a novel member of
A:\Genetics: 2; Genes: 1
A:\Gene: ch gamma-c-a

Query Match 33.2%; Score 427.5; DB 2; Length 348;
Best Local Similarity 42.9%; Pred. No. 3.5e-28;
Matches 91; Conservative 36; Mismatches 56; Indels 29; Gaps 9;

2Y 34 PLPE-VQCFVFNVMNCTWSSSPQPTNLTLYWYKNSDNDKVKQCSHYLSERITSG 92
DB 24 PSFGVECLIFEEYMTCTW-GSGQTLTANSLYLYWYEN--KLPVVCQOYLWDRSVRIG 80
2Y 93 COLQKEIHLVQTFVVO-----LQDPREPRQATQMLKQNLVWPAPENLTLLHL 143
DB 81 CFPESEIIQFAFVRVNASCGQTEIP-----SNRMELQNLVWPAPVNLTHNM 133
2Y 144 SSQLELNNRRF-LNHCLHLVQYRTDWDHSWTEQSDVYRHK---PSLSPVDGQKRYTF 199
DB 134 SQNLQTLTWSSPYKPEQCLHVVYKSKNDTSWTNOEV---XGVIFSPFSDVYKYYTF 189
2Y 200 VYRSFNPFCGSAQHSWSPHPHWGNS-TSK 230
DB 190 YYRSKINNYCGNTQLMSEWSPVFWGNNSTSK 221

RESULT 5
JC7773
IL-13ralpha 1 protein - rat
C:\Species: Rattus norvegicus (Norway rat)
C:\Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:\Accession: JC7773
R:\Pierrot, C.; Beniguel, L.; Beque, A.; Khalife, J.
Biochem. Biophys. Res. Commun. 287, 969-976, 2001
A:\Title: Expression of a functional IL-13ralpha by rat B cells.
A:\Reference number: JC7773; PMID:11573960
A:\Accession: JC7773
A:\Molecule type: mRNA
A:\Residues: 1-426 <PIE>
A:\Cross-references: GB:AY044251
A:\Comment: This protein is an functionally binding protein involved in B cell proliferation
A:\Genetics: 2; Genes: 1
A:\Gene: il-13ralpha

Query Match 13.1%; Score 168.5; DB 2; Length 426;
Best Local Similarity 25.5%; Pred. No. 1.7e-06;
Matches 54; Conservative 30; Mismatches 101; Indels 27; Gaps 8;

2Y 37 EQVCFVFNVMNCTWSSSPQPTNLTLYWYKNSDNDKVKQCSHYLSERITSGCQL 95
DB 129 ELQCTWNLSTYKCSWLPKQNTSPDNTLTLYWY--SSLGKSLQCEH-IHQCHIGCSF 185
2Y 96 QKKEI---HLVQTFVVOQDPREPRQATQMLKQNLVWPAPENLTLLHLKLSQLELAW 152
DB 186 KLTKVESYNEHHNIQIMWKDAGKIRPSYKIVTSNPKPGPHIKLF-LKNGALFVQW 244
2Y 153 NN--RFLNHCLHLVQYRT

C:\Species: Gallus gallus (chicken)
C:\Date: 03-Feb-2003 #sequence_revision 03-Feb-2003 #text_change 31-Mar-2003
C:\Accession: JC7907
R:\Min, W.; Lillehoj, H.S.; Fetterer, R.H.
Biochem. Biophys. Res. Commun. 299, 321-327, 2002
A:\Title: Identification of an alternatively spliced isoform of the common cytokine receptor
A:\Reference number: JC7907; MUID:23225486; PMID:12437989
A:\Accession: JC7907
A:\Molecule type: mRNA
A:\Residues: 1-348 <MIN>
A:\Cross-references: GB:AJ419897; GB:AJ419898
A:\Experimental source: egg
A:\Comment: This protein, expressed as a transmembrane glycoprotein, is a novel member of
A:\Genetics: 2; Genes: 1
A:\Gene: ch gamma-c-a

Query Match 33.2%; Score 427.5; DB 2; Length 348;
Best Local Similarity 42.9%; Pred. No. 3.5e-28;
Matches 91; Conservative 36; Mismatches 56; Indels 29; Gaps 9;

2Y 34 PLPE-VQCFVFNVMNCTWSSSPQPTNLTLYWYKNSDNDKVKQCSHYLSERITSG 92
DB 24 PPKGVCEILFEIYYMTCTW-GSGQTLTANSLYLYWYEN--KLPVVCQOYLWDRSVRIG 80
2Y 93 COLOKKEIHLVQTFVVO-----LQDPREPRQATQMLKQNLVWPAPENLTLLHKL 143
DB 81 CFPEQSEIIQFAFVVRVNASCNQGTLEIP-----SNRMELQNLVWPAPVNLTHNM 133
2Y 144 SSSQLELNNRRF-LNHCLHLVQYRTDWDHSWTEQSVYRHK---FSLSPVDGQKRYTF 199
DB 134 SQNQLQTLWSSPYKPEQCLEHVVYKSKNDTSWTNOEV---KGVIFSPFSDVYKYYTF 189
2Y 200 VYRSFNFPLCGSAQHSWSPHPHWGNS-TSK 230
DB 190 YYRSKINNYCGNTQLWSEWSPVFWGNNSTSK 221

RESULT 5
JC7773
IL-13ralpha 1 protein - rat
C:\Species: Rattus norvegicus (Norway rat)
C:\Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:\Accession: JC7773
R:\Pierrot, C.; Beniguel, L.; Beque, A.; Khalife, J.
Biochem. Biophys. Res. Commun. 287, 969-976, 2001
A:\Title: Expression of a functional IL-13ralpha by rat B cells.
A:\Reference number: JC7773; PMID:11573960
A:\Accession: JC7773
A:\Molecule type: mRNA
A:\Residues: 1-426 <PIE>
A:\Cross-references: GB:AY044251
A:\Comment: This protein is an functionally binding protein involved in B cell proliferation
A:\Genetics: 2; Genes: 1
A:\Gene: il-13ralpha

Query Match 13.1%; Score 168.5; DB 2; Length 426;
Best Local Similarity 25.5%; Pred. No. 1.7e-06;
Matches 54; Conservative 30; Mismatches 101; Indels 27; Gaps 8;

2Y 37 EVOCFVFNVMNCTWSSSPQPTNLTLYWYKNSDNDKVKQCSHYLSERITSGCQL 95
DB 129 ELQCTWNLSTYKCSWLPKQKTSPTDNTLYWY--SSLGKSLQCEH-IHQCHIGCSF 185
2Y 96 QKKEI---HLVQTFVVOQDPREPRQATQMLKQNLVWPAPENLTLLHKLSSQLELAW 152
DB 186 KLTKVESYNEHHNIQIMWKDAGKIRPSYKIVTSNPKPGPHIKLF-LKNGALFVQW 244
2Y 153 NN--RFLNHCLHLVQYRTDWDHSWTEQSVYRHK-----FSLSPVDGQ 194
DB 245 KNPQFSSRCLSYEVEVNSTQDTSNLSLEVBEDKQCNSEFDRNMEGASCFISPGVLXN 304
195 KRYTFVRSFNFPLC-GSAQHSWSPHPHWG 225

C:\Species: Gallus gallus (chicken)
C:\Date: 03-Feb-2003 #sequence_revision 03-Feb-2003 #text_change 31-Mar-2003
C:\Accession: JC7907
R:\Min, W.; Lillehoj, H.S.; Fetterer, R.H.
Biochem. Biophys. Res. Commun. 299, 321-327, 2002
A:\Title: Identification of an alternatively spliced isoform of the common cytokine receptor
A:\Reference number: JC7907; MUID:23225486; PMID:12437989
A:\Accession: JC7907
A:\Molecule type: mRNA
A:\Residues: 1-348 <MIN>
A:\Cross-references: GB:AJ419897; GB:AJ419898
A:\Experimental source: egg
A:\Comment: This protein, expressed as a transmembrane glycoprotein, is a novel member of
A:\Genetics: 2; Genes: 1
A:\Gene: ch gamma-c-a

Query Match 33.2%; Score 427.5; DB 2; Length 348;
Best Local Similarity 42.9%; Pred. No. 3.5e-28;
Matches 91; Conservative 36; Mismatches 56; Indels 29; Gaps 9;

2Y 34 PLPE-VQCFVFNVMNCTWSSSPQPTNLTLYWYKNSDNDKVKQCSHYLSERITSG 92
DB 24 PPKGVCEILFEIYYMTCTW-GSGQTLTANSLYLYWYEN--KLPVVCQOYLWDRSVRIG 80
2Y 93 COLOKKEIHLVQTFVVO-----LQDPREPRQATQMLKQNLVWPAPENLTLLHKL 143
DB 81 CFPEQSEIIQFAFVVRVNASCNQGTLEIP-----SNRMELQNLVWPAPVNLTHNM 133
2Y 144 SSSQLELNNRRF-LNHCLHLVQYRTDWDHSWTEQSVYRHK---FSLSPVDGQKRYTF 199
DB 134 SQNQLQTLWSSPYKPEQCLEHVVYKSKNDTSWTNOEV---KGVIFSPFSDVYKYYTF 189
2Y 200 VYRSFNFPLCGSAQHSWSPHPHWGNS-TSK 230
DB 190 YYRSKINNYCGNTQLWSEWSPVFWGNNSTSK 221

RESULT 5
JC7773
IL-13ralpha 1 protein - rat
C:\Species: Rattus norvegicus (Norway rat)
C:\Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:\Accession: JC7773
R:\Pierrot, C.; Beniguel, L.; Beque, A.; Khalife, J.
Biochem. Biophys. Res. Commun. 287, 969-976, 2001
A:\Title: Expression of a functional IL-13ralpha by rat B cells.
A:\Reference number: JC7773; PMID:11573960
A:\Accession: JC7773
A:\Molecule type: mRNA
A:\Residues: 1-426 <PIE>
A:\Cross-references: GB:AY044251
A:\Comment: This protein is an functionally binding protein involved in B cell proliferation
A:\Genetics: 2; Genes: 1
A:\Gene: il-13ralpha

Query Match 13.1%; Score 168.5; DB 2; Length 426;
Best Local Similarity 25.5%; Pred. No. 1.7e-06;
Matches 54; Conservative 30; Mismatches 101; Indels 27; Gaps 8;

2Y 37 EVOCFVFNVMNCTWSSSPQPTNLTLYWYKNSDNDKVKQCSHYLSERITSGCQL 95
DB 129 ELQCTWNLSTYKCSWLPKQKTSPTDNTLYWY--SSLGKSLQCEH-IHQCHIGCSF 185
2Y 96 QKKEI---HLVQTFVVOQDPREPRQATQMLKQNLVWPAPENLTLLHKLSSQLELAW 152
DB 186 KLTKVESYNEHHNIQIMWKDAGKIRPSYKIVTSNPKPGPHIKLF-LKNGALFVQW 244
2Y 153 NN--RFLNHCLHLVQYRTDWDHSWTEQSVYRHK-----FSLSPVDGQ 194
DB 245 KNPQFSSRCLSYEVEVNSTQDTSNLSLEVBEDKQCNSEFDRNMEGASCFISPGVLXN 304
195 KRYTFVRSFNFPLC-GSAQHSWSPHPHWG 225

C:\Species: Gallus gallus (chicken)
C:\Date: 03-Feb-2003 #sequence_revision 03-Feb-2003 #text_change 31-Mar-2003
C:\Accession: JC7907
R:\Min, W.; Lillehoj, H.S.; Fetterer, R.H.
Biochem. Biophys. Res. Commun. 299, 321-327, 2002
A:\Title: Identification of an alternatively spliced isoform of the common cytokine receptor
A:\Reference number: JC7907; MUID:23225486; PMID:12437989
A:\Accession: JC7907
A:\Molecule type: mRNA
A:\Residues: 1-348 <MIN>
A:\Cross-references: GB:AJ419897; GB:AJ419898
A:\Experimental source: egg
A:\Comment: This protein, expressed as a transmembrane glycoprotein, is a novel member of
A:\Genetics: 2; Genes: 1
A:\Gene: ch gamma-c-a

Query Match 33.2%; Score 427.5; DB 2; Length 348;
Best Local Similarity 42.9%; Pred. No. 3.5e-28;
Matches 91; Conservative 36; Mismatches 56; Indels 29; Gaps 9;

2Y 34 PLPE-VQCFVFNVMNCTWSSSPQPTNLTLYWYKNSDNDKVKQCSHYLSERITSG 92
DB 24 PPKGVCEILFEIYYMTCTW-GSGQTLTANSLYLYWYEN--KLPVVCQOYLWDRSVRIG 80
2Y 93 COLOKKEIHLVQTFVVO-----LQDPREPRQATQMLKQNLVWPAPENLTLLHKL 143
DB 81 CFPEQSEIIQFAFVVRVNASCNQGTLEIP-----SNRMELQNLVWPAPVNLTHNM 133
2Y 144 SSSQLELNNRRF-LNHCLHLVQYRTDWDHSWTEQSVYRHK---FSLSPVDGQKRYTF 199
DB 134 SQNQLQTLWSSPYKPEQCLEHVVYKSKNDTSWTNOEV---KGVIFSPFSDVYKYYTF 189
2Y 200 VYRSFNFPLCGSAQHSWSPHPHWGNS-TSK 230
DB 190 YYRSKINNYCGNTQLWSEWSPVFWGNNSTSK 221

RESULT 5
JC7773
IL-13ralpha 1 protein - rat
C:\Species: Rattus norvegicus (Norway rat)
C:\Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:\Accession: JC7773
R:\Pierrot, C.; Beniguel, L.; Beque, A.; Khalife, J.
Biochem. Biophys. Res. Commun. 287, 969-976, 2001
A:\Title: Expression of a functional IL-13ralpha by rat B cells.
A:\Reference number: JC7773; PMID:11573960
A:\Accession: JC7773
A:\Molecule type: mRNA
A:\Residues: 1-426 <PIE>
A:\Cross-references: GB:AY044251
A:\Comment: This protein is an functionally binding protein involved in B cell proliferation
A:\Genetics: 2; Genes: 1
A:\Gene: il-13ralpha

Query Match 13.1%; Score 168.5; DB 2; Length 426;
Best Local Similarity 25.5%; Pred. No. 1.7e-06;
Matches 54; Conservative 30; Mismatches 101; Indels 27; Gaps 8;

2Y 37 EVOCFVFNVMNCTWSSSPQPTNLTLYWYKNSDNDKVKQCSHYLSERITSGCQL 95
DB 129 ELQCTWNLSTYKCSWLPKQKTSPTDNTLYWY--SSLGKSLQCEH-IHQCHIGCSF 185
2Y 96 QKKEI---HLVQTFVVOQDPREPRQATQMLKQNLVWPAPENLTLLHKLSSQLELAW 152
DB 186 KLTKVESYNEHHNIQIMWKDAGKIRPSYKIVTSNPKPGPHIKLF-LKNGALFVQW 2


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C;Species: Rattus sp. (rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 27-Oct-2003
C;Accession: I56563
R;Appel, K.; Butini, M.; Sauter, A.; Gebicke-Haerter, P.J.
J. Neurosci. 15, 5800-5809, 1995
A;Title: Cloning of rat interleukin-3 receptor beta-subunit from cultured microglia and
A;Reference number: I56563; MUID:95370942; PMID:7643220
A;Accession: I56563
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-896 <RES>
A;Cross-references: GB:S79263; NID:gl086954; PIDN:AAB35068.1; PID:gl086955
C;Genetics:
C;Gene: IL-3rbeta
C;Superfamily: interleukin (IL)-3/IL-5/GM-CSF receptor common beta chain; cytokine recep
C;Keywords: cytokine receptor
F;39-235/Domain: cytokine receptor homology <CRS1>
F;253-433/Domain: cytokine receptor homology <CRS2>

Query Match 10.6%; Score 136.5; DB 2; Length 896;
Best Local Similarity 23.9%; Pred. No. 0.0019;
Matches 48; Conservative 41; Mismatches 83; Indels 29; Gaps 11;

QY 38 VQCFVFNVEYMNCTWNSSEPOPTNLTLHYWKNSDNDKVKCQSHYLFSEITSG----- 92
DB 251 LQCFPDGQSLNCSNEVNIK-VTDSVSGLFSSPKAGEKKCSFVV--KELQASRYTRY 307
QY 93 -COLQKKEIHLYQTFVVOLOQDPREPRQATQMLKQLNVLIPWAPENLTLLKLSOLELN 151
DB 308 HCSLNVSDPAHSAQYTSVK-----RLQGFIESFN-HIQWNPPTLNLTKNRDS-YSLH 360
QY 152 WNNR-----FLNLCLEHLVOYRTD---WDHSWTEQSDVYRKPSLPSVDGQKRYTFVRVS 203
DB 361 WETQKMSYPPFOHAFQ--VOYKKLDRWEDSKTE-NLNHAHMDLPQLEPGTSCARVRV 417
QY 204 RFNPLCGSAQHWSEWSHPH 224
DB 418 KTIPEYKGL--WSEWSNCTW 436

RESULT 11
S50040
N;Alternate names: GM-CSF receptor alpha-3 chain - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
C;Accession: S50040; S47568
R;Hu, X.; Zuckerman, K.S.
submitted to the EMBL Data Library, March 1994
A;Description: Cloning and sequencing of the cDNA encoding alternative splicing variants
A;Reference number: S50039
A;Accession: S50040
A;Molecule type: mRNA
A;Residues: 1-378 <HUX>
A;Cross-references: EMBL:L29349; NID:9460284; PIDN:AAA60962.1; PID:9463107
R;Hu, X.; Emanuel, P.D.; Zuckerman, K.S.
Biochim. Biophys. Acta 1223, 306-308, 1994
A;Title: Cloning and sequencing of the cDNA encoding two alternative splicing-derived v
A;Reference number: S47567; MUID:9436898; PMID:8086503
A;Accession: S47568
A;Molecule type: mRNA
A;Residues: 241-315,317-378 <HW>
A;Cross-references: EMBL:L29349
C;Genetics:
A;Gene: GM-CSF-RA3; CSF3RA
A;Introns: 316/3
C;Keywords: alternative splicing; glycoprotein; growth factor receptor; transmembrane pr
Query Match 10.5%; Score 135.5; DB 2; Length 378;
Best Local Similarity 20.5%; Pred. No. 0.00081;
Matches 50; Conservative 43; Mismatches 90; Indels 61; Gaps 10;

QY 5 ILTPN-GNEDTTADFFLTMTDLSVSTLPLPVCQFVFNVEYMNCTWNSSEPPQPTNL 63

C;Species: Rattus sp. (rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 27-Oct-2003
C;Accession: I56563
R;Appel, K.; Butini, M.; Sauter, A.; Gebicke-Haerter, P.J.
J. Neurosci. 15, 5800-5809, 1995
A;Title: Cloning of rat interleukin-3 receptor beta-subunit from cultured microglia and
A;Reference number: I56563; MUID:95370942; PMID:7643220
A;Accession: I56563
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-896 <RES>
A;Cross-references: GB:S79263; NID:gl086954; PIDN:AAB35068.1; PID:gl086955
C;Genetics:
C;Gene: IL-3rbeta
C;Superfamily: interleukin (IL)-3/IL-5/GM-CSF receptor common beta chain; cytokine recep
C;Keywords: cytokine receptor
F;39-235/Domain: cytokine receptor homology <CRS1>
F;253-433/Domain: cytokine receptor homology <CRS2>

Query Match 10.3%; Score 132.5; DB 2; Length 830;
Best Local Similarity 22.2%; Pred. No. 0.0037;
Matches 44; Conservative 37; Mismatches 96; Indels 21; Gaps 7;

QY 38 VQCFVFNVEYMNCTWNSSE-POPTNLTLHYWKNSDNDKVKCQSHYLFSEITSGCOLQ 96
DB 34 ICRSLKETFTSCWKPGSDGGLPTNYTL--FYSKDSEKIYECPDYGMWG--PNSCYFD 89
QY 97 KKEIHLYQTFVVOLOQDPREPRQAT--QMLKQLNVLIPWAPENLTLLH---KLSSOLELN 151
DB 90 KNTNPWTITNYITVAMNEIGSNSSDPQYVDVTSIVQPDAPVNLSTETKSASTYLLAK 149
QY 152 WNNRFL-----NHCLEHLVQYRTDWDHSWTEQSDVYRKPSLPSVDGQKRYTFVRSRF 205
DB 150 WSPFPPLADVTSNHYRYELRLKPEKEWETVSGVQTKVNRLOAGVYVVOVRCVL 209
QY 206 NFLCGSAQHWSEWSHPH 223
DB 210 D-----IGWSEWSSERH 222

RESULT 13
A33380
interleukin-4 receptor precursor - mouse
N;Alternate names: IL-4 receptor
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 01-Dec-2000
R;Mosley, B.; Beckmann, M.P.; March, C.J.; Idzerda, R.L.; Gimpel, S.D.; VandenBos, T.; F
Widmer, M.B.; Cosman, D.; Park, L.S.
Cell 59, 335-348, 1989
A;Title: The murine interleukin-4 receptor: molecular cloning and characterization of se
A;Reference number: A30911; MUID:90030408; PMID:2805066
A;Accession: A33380

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```
A: Molecule type: mRNA
A: Residues: 1-810 <MOI>
A: Cross-references: GB:M27959; NID:G198363; PIDN:AAA39299.1; PID:G309408
A: Accession: B33380
A: Molecule type: mRNA
A: Residues: 1-258 <MO2>
A: Accession: C33380
A: Molecule type: mRNA
A: Residues: 1-224, 'PSNENL' <MO3>
A: Cross-references: GB:M27960; NID:G198365; PIDN:AAA39300.1; PID:G309409
A: Note: part of this sequence, including the amino end of the mature protein, was confirmed by three forms of cDNA were isolated; the longest encodes extracellular, transmembrane and may encode a soluble form of the receptor
A: Harada, N.; Castle, B.E.; Gorman, D.M.; Itoh, N.; Schreurs, J.; Barrett, R.L.; Howard, Proc. Natl. Acad. Sci. U.S.A. 87, 857-861, 1990
A: Title: Expression cloning of a cDNA encoding the murine interleukin 4 receptor based on
A: Reference number: A34861; MUID:90138976; PMID:2405398
A: Accession: A34861
A: Molecule type: mRNA
A: Residues: 1-810 <HAR>
A: Cross-references: GB:M29854; NID:G198346; PIDN:AAA39297.1; PID:G309407
A: Wrighton, N.C.; Campbell, L.A.; Lee, F.D.
Growth Factors 6, 103-118, 1992
A: Title: The murine interleukin-4 receptor gene: Genomic structure, expression and potential
A: Reference number: 154232; MUID:92265335; PMID:1534014
A: Accession: 154232
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 1-73, '1', 75-333, 'P', 335-810 <RES>
A: Cross-references: GB:M48479; NID:G198359; PIDN:AA59727.1; PID:G198361
C: Geneticks:
A: Introns: 24/1; 71/2; 122/1; 172/3; 225/1; 258/2; 284/3; 301/2
A: Superfamily: interleukin-4 receptor; cytokine receptor homology
C: Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein
F: 1-25/Domain: signal sequence #status predicted <SIG>
F: 26-810/Product: interleukin-4 receptor #status experimental <MAT>
F: 26-233/Domain: extracellular #status predicted <EXT>
F: 24-219/Domain: cytokine receptor homology <CRS>
F: 234-257/Domain: transmembrane #status predicted <TMM>
F: 258-810/Domain: intracellular #status predicted <INT>
F: 72,129,135,163,177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.2%; Score 132; DB 1; Length 810;
Best Local Similarity 26.2%; Pred. No. 0.004;
Matches 60; Conservative 28; Mismatches 107; Indels 34; Gaps 8;

QY 14 TTADPFLTMTDTSLSVSTLPPEVQCFVFNVEYNNCTW-NSSSEPOPTNLTLHYWYKNS 72
D 10 TSVGCLILLVTGSGIKVLGSP--TCPSDYRTSTCEWFLDSDAVDCSSQLCLHY----- 62
QY 73 DNDKVKQCSHYLFSEIT-----SCQLOKKEIHLVQTFVVLQDPREPRQATQML 124
D 63 -----RLMFFESNLTICIPNSASTVCVCHMENRVPQSDRYQMELWAHRLQWQSP 116
QY 125 KLQNLVLPWAPENLTLKLSQSLNWNFLNHL--EHLVQY---RTDWDHSWTEQ 178
D 117 SPFGNVKPLADPNLTLHTNVSDEWLTWNLYPSNNLLKDLISWNISREDNPAEFIV 176
QY 179 SVDY---RHKFLSPVDGQKRYTFRRSRFPNPLCGSAGHSEWSPPIHW 224
D 177 NVTYKEPLSPFINTILMGSGVYVYARVRSQILTGT---WSESPSITW 222

RESULT 14
A35782
Cytokine receptor common beta chain precursor - mouse
C: Species: Mus musculus (house mouse)
C: Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 27-Oct-2003
C: Accession: A35782
R: Gorman, D.M.; Itoh, N.; Kitamura, T.; Schreurs, J.; Yonehara, S.; Yahara, I.; Arai, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 5459-5463, 1990
A: Title: Cloning and expression of a gene encoding an interleukin 3 receptor-like protei
A: Reference number: A35782; MUID:9013131; PMID:1695379

A: Accession: A35782
A: Molecule type: mRNA
A: Residues: 1-896 <GOR>
A: Cross-references: GB:M34397; NID:G191821; PIDN:AAA37204.1; PID:G309101
C: Comment: Mouse high-affinity IL-5, GM-CSF, and one class of high-affinity IL-3 recepto
C: Superfamily: interleukin (IL)-3/IL-5/GM-CSF receptor common beta chain; cytokine recei
C: Keywords: cytokine receptor; duplication; transmembrane protein
F: 1-22/Domain: signal sequence #status predicted <SIG>
F: 23-896/Product: cytokine receptor common beta chain #status predicted <MAT>
F: 23-441/Domain: extracellular #status predicted <EXT>
F: 39-235/Domain: cytokine receptor homology <CRS1>
F: 253-434/Domain: cytokine receptor homology <CRS2>
F: 442-463/Domain: transmembrane #status predicted <TMM>
F: 464-896/Domain: intracellular #status predicted <INT>

Query Match 9.7%; Score 125; DB 1; Length 896;
Best Local Similarity 23.1%; Pred. No. 0.017;
Matches 48; Conservative 36; Mismatches 82; Indels 42; Gaps 11;

QY 38 VOCFVFNVEYNNCTWSSSEPOPTNLTLHYWYKNSDNDKVKQCSHYLFSEITSGCQLQK 97
D 251 LQCFPDGIGSLHCSMEVWTQ-TTGSVSFGLFRPSPVAPEKCSFV----- 296
QY 98 KE---IHLVQTFVVLQDPREPRQATQMLKQLNV-----IPWAPENLTLHKLS 144
D 297 YTFRRSRFPNPLCGSAGHSEWSPPIHW 224
QY 145 ESQLELNWNR-----FLNHCLHVLVQY---TDWDHSWTEQSVQDYRHKFLSPVDGQKR 196
D 356 DS-YSLHWETQKWAYSFIEHTFQ--VOYKKKSDSWEDSKTB-NLDRAHSMDSLQLEPDT 411
QY 197 YTFRRSRFPNPLCGSAGHSEWSPPIHW 224
D 412 YCARVRVK--PISNYDGIWSKWSSEYTW 437

RESULT 15
I45971
Prolactin receptor - bovine
C: Species: Bos primigenius taurus (cattle)
C: Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Jul-2000
C: Accession: I45971
R: Scott, P.; Kessler, M.A.; Schuler, L.A.
Mol. Cell. Endocrinol. 89, 47-58, 1992
A: Title: Molecular cloning of the bovine prolactin receptor and distribution of prolact
A: Reference number: I45971; MUID:93246019; PMID:1338725
A: Accession: I45971
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: mRNA
A: Residues: 1-581 <SCO>
A: Cross-references: GB:L02549; NID:G163617; PIDN:AAA51417.1; PID:G163618
C: Geneticks:
A: Gene: PRLR
C: Superfamily: cytokine receptor homology
F: 36-221/Domain: cytokine receptor homology <CRS>

Query Match 9.4%; Score 121.5; DB 2; Length 581;
Best Local Similarity 25.4%; Pred. No. 0.02;
Matches 60; Conservative 30; Mismatches 69; Indels 77; Gaps 17;

QY 28 LSVSTL---PLPE---VQCFVFNVEYNNCTWSSSE-PQPTNLTLHYWYKNSDNDKVKQ 79
D 17 LSVSLNGOSPPEKPKLVKCRSPGKETTCWPEGAGGLPNTYLTLY-HKEGET-LIHE 74
QY 80 CSHYLFSEITSG---CQLQKKEIHLVQTFVVLQ-----QDPR-----EPRR 118
D 75 CPDYK-----TGPNSCYFSKCHTSIKWYVITVNAIQMGISSSDPLYVHVTVIPEPEP 129
QY 119 QATQMLKQY-----LVIPWAPENLTLKLSQSLNWNFLNHLCHLHVQY--- 168
D 130 PANLTLELKHPEKPKYLIKWSPPPTMT-----DVKSGW-----FIQYETRL 172
QY 169 -----TDWDHSWTEQSVQDYRHKFLSPVDGQKRYTFRRSRFPNPLCGSAGHSEWSP 219
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Db 173 KPEKATDWEHTLTKOTLK-IFNL--YFGQX---YLVQIRCKPDHG---YWSEWS 219

Search completed: March 3, 2004, 12:38:59
Job time : 16.5425 secs

Result	No.	Query			DB	ID	Description
		Score	Match	Length			
1	997.5	77.4	368	6	Q8SQ71	Q8sq71 sus scrofa	
2	919	71.4	278	11	Q8VHR8	Q8vhr8 rattus norv	
3	667.5	51.8	448	11	Q7TP53	Q7tp53 rattus norv	
4	427.5	33.2	348	13	Q8AUP2	Q8aup2 gallus gall	
5	427.5	33.2	374	13	Q8AV07	Q8av07 gallus gall	
6	283.5	22.0	343	13	Q9DEQ1	Q9deq1 oncorhynch	
7	279.5	21.7	313	13	Q8AJD1	Q8ajd1 oncorhynch	
8	259.5	20.1	404	13	Q90XP8	Q90xp8 oncorhynch	
9	213	16.5	385	6	Q95JF0	Q95jfo canis famli	
10	244.5	15.9	385	11	Q8VHK6	Q8vnh6 rattus norv	
11	193.5	15.5	383	11	Q8N786	Q8n786 mus musculu	
12	183.5	14.2	424	11	Q8BNM4	Q8bnm4 mus musculu	
13	181.5	14.1	424	11	Q8C1Z3	Q8c1z3 mus musculu	
14	181.5	14.1	442	11	Q7TT27	Q7tt27 mus musculu	
15	178	13.8	427	4	Q96BB4	Q96bb4 homo sapien	
16	177	13.7	409	6	Q7YRV5	Q7yrv5 macaca fasc	


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Db 23 LNPVKVLTSGNEDTADFLLLSTPPTGLNVSTLPLPKVQCFFVNFVYVNCVTWNSSELQP 82
QY 61 TNLTHYWKNSNDKVKQKSHYLFSEETSGCQKKEIHLYQTFVVOLODPPRQQA 120
Db 83 TNLTHYWKTSNDKVKQKSHYLFSEETSGCQKKEIRLYQTFVVOLODPPRQD 142
QY 121 TQMLKQNLVLPWAPENLTLHLKLSQLELNWNNRFLNHLCHLHVQYRTDWDHSTEQSV 180
Db 143 PQTLKQDLVLPWAPENLTLHLKLSQLELNWNNRFLNHLCHLHVQYRTDWDHSTEQSV 202
QY 181 DYHFKPSLPSVDQKRYTFRVRSRNPFLCGSAQHWSEWSPHIHWSNTSKEN 232
Db 203 DHRQSPSLPSVDAQKLYTFRVRSRNPFLCGSAQHWSDWSPHIHWSNTSKEN 253

RESULT 2
Q8VHR8 PRELIMINARY; PRT; 278 AA.
AC Q8VHR8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytokine receptor gamma chain (Fragment).
GN I12RG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Oloz F., Malek T.R.;
RA Chai L.Q., Yuan J.Y., Yang K.J., Van H.M., Chang C.P., Zhao L.F.,
RA Ma H., Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
RT "Liver regeneration after PH.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY325195; AAP92596.1; -.
DR EMBL; AY325195; AAP92596.1; -.
SQ SEQUENCE 278 AA; 51863 MW; 4011F8F774804CDD CRC64;

Query Match 71.4%; Score 919; DB 11; Length 278;
Best Local Similarity 70.6%; Pred. No. 8.6e-79;
Matches 163; Conservative 33; Mismatches 35; Indels 0; Gaps 0;

QY 2 NTTILTPNGNEDTADFFLTMTDLSVSTLPLPEVQCFVNFVYVNCVTWNSSEPOPT 61
Db 2 SSKVLLSSGNETKSDLLTSDMLKLSVPTLPLPEVQCFVNFVYVNCVTWNSSEPOPT 61
QY 62 NTLTHYWKNSNDKVKQKSHYLFSEETSGCQKKEIHLYQTFVVOLODPPRQQA 121
Db 62 NLTMYRYKSGSDNTFQECSHYLFSEETSGCQKKEIHLYQTFVVOLODPPRQAA 121
QY 122 QMLKQNLVLPWAPENLTLHLKLSQLELNWNNRFLNHLCHLHVQYRTDWDHSTEQSV 181
Db 122 OKLNLQNLVLPWAPENLTLHLKLSQLELNWNNRFLNHLCHLHVQYRTDWDHSTEQSV 181
QY 182 YHFKPSLPSVDQKRYTFRVRSRNPFLCGSAQHWSEWSPHIHWSNTSKEN 232
Db 182 HEHPSLPSVDQKLYTFRVRSRNPFLCGSTQWKSQPIHWSHTAEEN 232

RESULT 3
Q7TP53 PRELIMINARY; PRT; 448 AA.
AC Q7TP53;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ab2-183.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu C.S., Li W.Q., Li Y.C., Wang L., Wang S.F., Han H.P., Wang G.P.,
RA Chai L.Q., Yuan J.Y., Yang K.J., Van H.M., Chang C.P., Zhao L.F.,
RA Ma H., Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
RT "Liver regeneration after PH.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY325195; AAP92596.1; -.
DR EMBL; AY325195; AAP92596.1; -.
SQ SEQUENCE 448 AA; 51863 MW; EBD56D1FA86614D5 CRC64;

Query Match 51.8%; Score 667.5; DB 11; Length 448;
Best Local Similarity 70.2%; Pred. No. 9.2e-55;
Matches 118; Conservative 26; Mismatches 23; Indels 1; Gaps 1;

QY 66 HYV-YXNSDNDKVKQKSHYLFSEETSGCQKKEIHLYQTFVVOLODPPRQQA 124
Db 21 HDWRYKSGSDNTFQECSHYLFSEETSGCQKKEIHLYQTFVVOLODPPRQAA 80
QY 125 KQNLVLPWAPENLTLHLKLSQLELNWNNRFLNHLCHLHVQYRTDWDHSTEQSV 184
Db 81 NLQNLVLPWAPENLTLHLKLSQLELNWNNRFLNHLCHLHVQYRTDWDHSTEQSV 140
QY 185 KFSPLPSVDQKRYTFRVRSRNPFLCGSAQHWSEWSPHIHWSNTSKEN 232
Db 141 RFSPLPSVDQKLYTFRVRSRNPFLCGSTQWKSQPIHWSHTAEEN 188

RESULT 4
Q8AUP2 PRELIMINARY; PRT; 348 AA.
AC Q8AUP2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative common cytokine receptor gamma chain a precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=white leghorn SC, and Leghorn; TISSUE=Liver, and Spleen;
RX MEDLINE=22325486; PubMed=12437989;
RA Min W., Lillehoj H.S., Fetterer R.H.;
RT "Identification of an alternatively spliced isoform of the common
cytokine receptor gamma, Greek chain in chickens.";
RL Biochem. Biophys. Res. Commun. 299:321-327(2002).
DR EMBL; AJ419897; CAD12042.1; -.
DR EMBL; AJ419898; CAD12043.1; -.
DR PIR; JC7907; JC7907.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR InterPro; IPR002996; CRJA.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR003531; Hemtopoptn_S_F1.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
DR Receptor.
KW Receptor.
FT NON TER 1
FT NON TER 278
SQ SEQUENCE 278 AA; 32719 MW; 4011F8F774804CDD CRC64;

Query Match 71.4%; Score 919; DB 11; Length 278;
Best Local Similarity 70.6%; Pred. No. 8.6e-79;
Matches 163; Conservative 33; Mismatches 35; Indels 0; Gaps 0;

QY 2 NTTILTPNGNEDTADFFLTMTDLSVSTLPLPEVQCFVNFVYVNCVTWNSSEPOPT 61
Db 2 SSKVLLSSGNETKSDLLTSDMLKLSVPTLPLPEVQCFVNFVYVNCVTWNSSEPOPT 61
QY 62 NTLTHYWKNSNDKVKQKSHYLFSEETSGCQKKEIHLYQTFVVOLODPPRQQA 121
Db 62 NLTMYRYKSGSDNTFQECSHYLFSEETSGCQKKEIHLYQTFVVOLODPPRQAA 121
QY 122 QMLKQNLVLPWAPENLTLHLKLSQLELNWNNRFLNHLCHLHVQYRTDWDHSTEQSV 181
Db 122 OKLNLQNLVLPWAPENLTLHLKLSQLELNWNNRFLNHLCHLHVQYRTDWDHSTEQSV 181
QY 182 YHFKPSLPSVDQKRYTFRVRSRNPFLCGSAQHWSEWSPHIHWSNTSKEN 232
Db 182 HEHPSLPSVDQKLYTFRVRSRNPFLCGSTQWKSQPIHWSHTAEEN 232

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```
Query Match      33.2%; Score 427.5; DB 13; Length 348;
Best Local Similarity 42.9%; Pred. No. 3.4e-32;
Matches 91; Conservative 36; Mismatches 56; Indels 29; Gaps 9;

QY 34 PLPE-VQCFVFNVEYMNCTWSSSEPPQPTNLTLYHYWYKNSDNDKVQKSHYLFSEETSG 92
DB 24 PSPKGVECLFNEEYMTCTW-GSGQTLTANYSLYYWYEN--KLPVVEQQYLWDRSVRIG 80
QY 93 COLQKEHLHYQTFVVO-----LQDPREPRAQATQMLKQLNLYVPWAPENLTLHLK 143
DB 81 CRFGESEIIQFAFYRVNASCNGQTLIP-----SNRMELQNLVKPEAPVNLTHNM 133
QY 144 SESQLELWNNRFLNHCHLEHLVQVTRTDHDSWTEQSDVYRHK---FSLPSVDGQKTYTF 199
DB 134 SGNQLQLTWSSPYPKQECLEHVYKSKNDTSWNQEV----KGVIFSPFSDVEKYTYTF 189
QY 200 RYRSRPNPLCGSAQHSWSHPHIGWSN-TSK 230
DB 190 YVRSKINNYCGNTQLWSEWSVFPWGNNSTSK 221

RESULT 5
QYAV07 PRELIMINARY; PRT; 374 AA.
AC Q8AV07;
DT 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Putative common cytokine receptor gamma chain b precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=white leghorn SC; TISSUE=Spleen;
RX MEDLINE=2325486; PubMed=12437989;
RA Min W., Lillehoj H.S., Fetterer R.H.;
RT "Identification of an alternatively spliced isoform of the common
RT cytokine receptor gamma, Greek chain in chickens.";
RL Biochem. Biophys. Res. Commun. 299:321-327(2002).
DR EMBL; AJ419896; CAD12041.1;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN.III.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
DR Signal; Receptor.
FT SIGNAL 1 21 POTENTIAL.
SQ SEQUENCE 374 AA; 42547 MW; B3A62E0D4D02B42B CRC64;

Query Match      33.2%; Score 427.5; DB 13; Length 374;
Best Local Similarity 42.9%; Pred. No. 3.7e-32;
Matches 91; Conservative 36; Mismatches 56; Indels 29; Gaps 9;

QY 34 PLPE-VQCFVFNVEYMNCTWSSSEPPQPTNLTLYHYWYKNSDNDKVQKSHYLFSEETSG 92
DB 24 PSPKGVECLFNEEYMTCTW-GSGQTLTANYSLYYWYEN--KLPVVEQQYLWDRSVRIG 80
QY 93 COLQKEHLHYQTFVVO-----LQDPREPRAQATQMLKQLNLYVPWAPENLTLHLK 143
DB 81 CRFGESEIIQFAFYRVNASCNGQTLIP-----SNRMELQNLVKPEAPVNLTHNM 133
QY 144 SESQLELWNNRFLNHCHLEHLVQVTRTDHDSWTEQSDVYRHK---FSLPSVDGQKTYTF 199
DB 134 SGNQLQLTWSSPYPKQECLEHVYKSKNDTSWNQEV----KGVIFSPFSDVEKYTYTF 189
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QY 200 RYRSRPNPLCGSAQHSWSHPHIGWSN-TSK 230
DB 190 YVRSKINNYCGNTQLWSEWSVFPWGNNSTSK 221

RESULT 6
QYDEQ1 PRELIMINARY; PRT; 343 AA.
AC Q9DEQ1;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Cytokine receptor common gamma chain.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21287902; PubMed=11394690;
RA Wang T., Secombes C.J.;
RT "Cloning and expression of a putative common cytokine receptor gamma
RT chain gene in rainbow trout (Oncorhynchus mykiss).";
RL Fish and Shellfish Immunol. 11:233-244(2001).
DR EMBL; AJ276623; CAC09429.2;
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003961; FN.III.
DR SMART; SM00060; FN3; 1.
DR Receptor.
SQ SEQUENCE 343 AA; 39486 MW; ED8429E7534B21EB CRC64;

Query Match      22.0%; Score 283.5; DB 13; Length 343;
Best Local Similarity 30.9%; Pred. No. 1.4e-18;
Matches 59; Conservative 37; Mismatches 88; Indels 7; Gaps 4;

QY 36 PEVQCFVFNVEYMNCTWSSSEPPQPTNLTLYHYWYKNSDNDKVQKSHYLFSEETSG 95
DB 23 PNVNCLINLDYVNCILWSEQSIPE-VNFT--FFSSRFKDNMECTTYLOESYAVGRL 79
QY 96 QKKEHLHYQTFVVOQLQDPREPRAQATQMLKQLNLYVPWAPENLTLHLKSEQLNWNRR 155
DB 80 SYDKSDRPTLTATKLIV--HQNNSVYVDHNLKSMVKLYPPVNLVSMNKDPELNLYMNS 136
QY 156 FLNCHLEHLVQVTRTDHDSWTEQSDVYRHKSLPSVDGQKTYTFVRSRPNPLCGSAQHW 215
DB 137 KNTFIESEVRYRINS-D-KWKTSTPSKQYAVAPPLKSSRYBFQVRAVNDMCGSEFW 195
QY 216 SEWSHPHIGWS 226
DB 196 SEWSQPIQWDS 206

RESULT 7
Q8JJD1 PRELIMINARY; PRT; 313 AA.
AC Q8JJD1;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Cytokine receptor common gamma chain precursor.
GN IL2RGAMMA.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Soma G., Inagawa H., Honda T., Nishizawa T., Kanou J., Endo M.,
RA Ootake M., Nakanishi T.;
RT "Rainbow trout cytokine receptor common gamma chain precursor (IL-2R
RT gamma chain) like protein.";
```

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB042024; BAB91242.1; --
DR GO; GO:0004872; F:receptor activity; IEA.
KW Signal; Receptor.
FT SIGNAL
SQ SEQUENCE 313 AA; 36259 MW; 28278777AF2F9BF2 CRC64;
POTENTIAL.
Query Match 21.7%; Score 279.5; DB 13; Length 313;
Best Local Similarity 30.4%; Pred. No. 2.9e-18;
Matches 58; Conservative 38; Mismatches 88; Indels 7; Gaps 4;
QY 36 PEVQCFVFNVEYVNCWSSSPQPTNLTLYHYKNSDNDKVKCSHYLFSSEITSGCOL 95
DB 23 PNVNCLINLVNCIWSQSIPV-VNFT--PFSSRFKIDNMEECTTYLQSDSVAVGRL 79
QY 96 OKKEHLVQTFVVLQDPRPRQATOMLKLQNLVLPWAPENLTLLKLSQLELNNR 155
DB 80 SYDKSDRFLLTKLV---HQNMSVQDHNLSKMKVLPVNLSEVMNKDPELNLWNNS 136
QY 156 FLNHGCHLVQYRTDWDHSHWTSQSDYDRKFLPSVDGQKRYTFRVSRFNPGLCSAQHW 215
DB 137 KNTFCIESEVRVINS-D-KWKTSTPSKEQYAVAFPLKSSRYEFQVRAVNDMCGSKFW 195
QY 216 SEWSHPIHWS 226
DB 196 SEWSQPIQWDS 206
RESULT 8
Q90XP8 PRELIMINARY; PRT; 404 AA.
AC Q90XP8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin 13 receptor alpha-2.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Procatopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Lockyer A.E., Jones C.S., Noble L.R., Verspoor E., Holland J.,
RA Secombes C.J.;
RT "Isolation and characterization of a putative interleukin 13 receptor
alpha-2 sequence from rainbow trout (Oncorhynchus mykiss).";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF361437; AAL26927.1; --
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR008957; FN_III-like.
KW Receptor.
SQ SEQUENCE 404 AA; 46728 MW; 4B9B7E3F4CFFB6D6 CRC64;
Query Match 20.1%; Score 259.5; DB 13; Length 404;
Best Local Similarity 27.9%; Pred. No. 3.1e-16;
Matches 56; Conservative 44; Mismatches 88; Indels 13; Gaps 6;
QY 40 CFVFNVEYVNCWSS-SPQPTNLTLYHYKNSDNDKVKCSHYLFSSEITSGCOLQK 98
DB 143 CVFYKEFMECTWETGLEPTQSQSLYFWHR--EMEQAECPQYIHNGVRTGCKFTE 200
QY 99 ETHLYQTF--VVLQDPRPRQATOMLKLQNLVLPWAPENLTLLKLSQLELNNW--N 153
DB 201 SUSEPFDNFCINSSPEVVLASAFSLQIQNYVPALETVHLEASDRLQVQWDLPN 260
QY 154 NPLNCLHLEHLVQYRTD--WDHSHWTSQSDYDRKFLPSVDGQKRYTFRVSRFNPGLCS 211
DB 261 ERIPRCHLEVEAREEGVGQGPLLQNVNTEWTLTSLMSDGAARKKCFVRVSRMHYCAD 320
QY 212 AQHSEWSHPIHWSNTSKEN 232

Db 321 RGFWSDWMS---HWSCHSDTES 338
RESULT 9
Q95LFO PRELIMINARY; PRT; 386 AA.
AC Q95LFO;
DT 01-DSC-2001 (TrEMBLrel. 19, Created)
DT 01-DSC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin 13 receptor alpha chain 2.
GN IL13RA2.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21287533; PubMed=11389954;
RA Tang L.;
RT "Molecular cloning of canine IL-13 receptor alpha chain (alpha1 and
alpha2) cDNAs and detection of corresponding mRNAs in canine
tissues";
RL Vet. Immunol. Immunopathol. 79:181-195(2001).
DR EMBL; AF314533; AAL14887.1; --
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain). ; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003532; Hemopoetin_S_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor.
SQ SEQUENCE 386 AA; 45110 MW; AL6FDF2DD023ED95 CRC64;
Query Match 16.5%; Score 213; DB 6; Length 386;
Best Local Similarity 25.8%; Pred. No. 7.3e-12;
Matches 61; Conservative 38; Mismatches 107; Indels 30; Gaps 8;
QY 3 TTILT-PNGNEDTADFLLTWTPTDSLSVSTPLPEVQCFVFNVEYVNCWSSSPQ-P 60
DB 125 TTYTSPQGNRET-----KIQDMCVYNNQYLVCWKPGMGVHFD 165
QY 61 TNLTLHYWYKNSDNDKVKCSHYLFSSEITSGCOLQKKEHLVQTFVVLQDPR--PRR 118
DB 166 TNYQLFWTEGLDHS--AECTYIKVNGKMGCRPYLESSDYKDFYICVNGSSSQPIR 223
QY 119 QATQMLKLQNLVLPWAPENLTLLKLSQLELNNW---NRFNLHCLHLEHLVQYRTDWDHSH 175
DB 224 PSYFIFQLQNLVVKMPDPYLSLTVKNSEINLKNWPKGPIPAKCFIYEIETED-GTWW 282
QY 176 TEQSDYRHKFLPSVDGQKRYTFRVSRFNPGLCSAQHSEWSHPIHWSNTSKE 231
DB 283 VTTVNEHQITRTSNESQK-LCFLVRSKNVNYCSDDGIGWSEWSDEQCKWGDINKE 337
RESULT 10
Q8VHK6 PRELIMINARY; PRT; 385 AA.
AC Q8VHK6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin 13 receptor alpha chain 2.
GN IL13RA2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Wu A., Low W.C.;

EMBL; BC015768; AAH15768.1; -.
EMBL; AL391280; CAD21446.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR002996; CR1A.
InterPro; IPR008957; FN_III-like.
InterPro; IPR003532; Hemtopoptn_S_F2.
PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
Receptor.
SEQUENCE 427 AA; 48676 MW; E6A42F7466A39A09 CRC64;
Query Match 13.8%; Score 178; DB 4; Length 427;
Best Local Similarity 26.7%; Pred. No. 1.7e-08;
Matches 58; Conservative 38; Mismatches 83; Indels 38; Gaps 11;
37 EVQCFVFNVEYNNCTWNSSEPOP-TNLTLHWYKNSDNDKVKCKSHYLFSEITSGC-- 93
131 ELQCIWHNLSYMKCSWLPGRNTSPDNTLYYWHRSI--EKIHQCEN-IFREGQYFGCSF 187
94 QLOKKEIHLVQTFVQL--QDPREPRQATOMLKLQNLVIPWAP--ENLTLHKLSESOLE 149
188 DLTAKVDSSEFQSHSVQIMVKDNAGKIKPSFNIVPLTSRVKPPDPPIKILSFH---NDLLY 244
150 LWNWN--RFLNHGLEHLVQYRTDMDHWT-----EOSVDYRHKFSLP 189
245 VQWENPQNFISRL-----FYEVENNSQTETHNVFYVQAEKCNPEFERNVENTSCFWVP 300
190 SVDGQKRYTFVRFSRNPIC-GSAQHWSEWSPHMG 225
301 GVLPDTLNTVRIKVTNKLCEYDDKLWNSWQMSIG 337

Search completed: March 3, 2004, 12:38:06
Job time : 39.9085 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 3, 2004, 12:24:04 ; Search time 55.3464 Seconds
(without alignments)
1184.377 Million cell updates/sec

Title: US-09-825-561A-4

Perfect score: 1288
Sequence: 1 LNTTILPENGNETADFFL.....QHWSESHPTWGSNTSKEN 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

1: geneseqp1980s.*

2: geneseqp1990s.*

3: geneseqp2000s.*

4: geneseqp2001s.*

5: geneseqp2002s.*

6: geneseqp2003as.*

7: geneseqp2003bs.*

8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1288	100.0	232	5	Aae13727 Human sol
2	1288	100.0	341	7	Abr61610 IL-2 comm
3	1288	100.0	347	2	Aar47149 IL-2 rece
4	1288	100.0	357	7	Abr61609 IL-2 comm
5	1288	100.0	360	5	Aae13734 Human sol
6	1288	100.0	369	2	Aar47148 IL-2 rece
7	1288	100.0	369	5	Aau96932 Human cyt
8	1288	100.0	369	6	Aau03612 Human exp
9	1288	100.0	369	6	Aau03613 Human exp
10	1288	100.0	369	6	Aau03602 Human exp
11	1288	100.0	369	6	Aau03603 Human exp
12	1288	100.0	369	6	Aau03605 Human exp
13	1288	100.0	369	6	Aau03600 Human exp
14	1288	100.0	369	6	Aau03601 Human exp
15	1288	100.0	691	3	Aay92202 Fusion po
16	1288	100.0	691	6	Aau03610 Human exp
17	1288	100.0	694	3	Aay92201 Fusion po
18	1288	100.0	694	3	Aay92203 Fusion po
19	1288	100.0	694	6	Aau03611 Human exp
20	1288	100.0	694	6	Aau03609 Human exp
21	1282	99.5	482	2	Aaw31646 Human cyt
22	1282	99.5	482	2	Aau03608 Human exp
23	1277	99.1	230	2	Aar47151 IL-2 rece
24	1277	99.1	252	2	Aar47150 IL-2 rece
25	1277	99.1	252	6	Aau03606 Human exp

26	1272	98.8	230	2	AAR82934	Aar82934 Interleuk
27	960	74.5	363	4	AAB71882	Aab71882 Bos tauru
28	854.5	66.3	369	2	AAR59094	Aar59094 Murine IL
29	853.5	66.3	369	5	Aau77221	Aau77221 Mouse com
30	542	42.1	121	3	AAG00283	Aag00283 Human sec
31	542	42.1	121	6	ABU03604	Abu03604 Human exp
32	215	16.7	561	4	Au69138	Au69138 Canine IL
33	215	16.7	561	4	Au69141	Au69141 Canine IL
34	215	16.7	563	4	Au69140	Au69140 Canine IL
35	215	16.7	563	4	Au69139	Au69139 Canine IL
36	213	16.5	318	4	Au69137	Au69137 Canine IL
37	213	16.5	365	4	Au69136	Au69136 Canine in
38	213	16.5	386	4	Au69135	Au69135 Canine in
39	207	16.1	315	2	Aaw56261	Aaw56261 Mature in
40	207	16.1	317	5	Aae13746	Aae13746 Human sol
41	207	16.1	359	2	Aaw56260	Aaw56260 Construct
42	207	16.1	380	2	Aaw36813	Aaw36813 Human Zcy
43	207	16.1	380	2	Aaw35295	Aaw35295 Human IL-
44	207	16.1	380	2	Aaw24972	Aaw24972 Human int
45	207	16.1	380	2	Aaw33603	Aaw33603 Homo sapi

ALIGNMENTS

RESULT 1

Aae13727

ID Aae13727 standard; protein; 232 AA.

AC Aae13727;

XX

XX

DT 26-FEB-2002 (first entry)

XX

DE Human soluble IL-2Rgamma cytokine receptor protein fragment.

XX Human; Zalphall; cytokine receptor; immunosuppressive; cytostatic;
 KW inflammatory disorder; haemostatic; cell proliferation; immune disorder;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
 KW myaschemia gravis; systemic lupus erythematosus; SLE; diabetes; aschma;
 KW ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis;
 KW viral infection; IL-2Rgamma.

XX Homo sapiens.

XX

XX

PN WO200177171-A2.

XX

PD 18-OCT-2001.

XX

XX 03-APR-2001; 2001WO-US010872.

XX

PR 05-APR-2000; 2000US-0194731P.

PR 28-JUL-2000; 2000US-0222121P.

XX

PA (ZYMO) ZYMOGENETICS INC.

XX

PI Sprechter CA, Novak JE, West JW, Presnell SR, Holly RD, Nelson AJ;

XX

DR WPI; 2002-025898/03.

DR N-PSDB; AAD22319.

XX

PT Novel soluble receptor polypeptides and polynucleotides used as cytokine

XX

PT antagonist for stimulating ligand activity-induced proliferation of

XX

PS hematopoietic cells and for suppressing immune response in a mammal.

XX

PS Claim 29; Page 175-176; 243pp; English.

XX

XX The invention relates to an isolated soluble zalphall cytokine receptor

CC polypeptide and their cDNA molecules. Zalph proteins are useful for

CC inhibiting or antagonising the ligand activity-induced proliferation of

CC haematopoietic cells and haematopoietic cell progenitors preferably

CC lymphoid cells which are natural killer cells or cytotoxic T cells.

CC Zalphall is useful for treating immune and inflammatory disorders, for

CC reducing proliferation of neoplastic B or T cells, for suppressing an

CC immune response in a mammal exposed to an antigen or pathogen. Zalpha is
 CC useful for treating diseases that require immune regulation including
 CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
 CC myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes;
 CC asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease,
 CC sepsis, viral infection (dengue virus infection) and cancer. The present
 CC sequence is human soluble IL-2Rgamma cytokine receptor cDNA fragment
 XX
 SQ Sequence 232 AA;

Query Match 100.0%; Score 1288; DB 5; Length 232;
 Best Local Similarity 100.0%; Pred. No. 3e-115;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTILTPNGNEDTTADFFLTMTDLSVSTLPLPEVOCFVFNVEYMNCTWNSSEPO 60
 DB 1 LNTTILTPNGNEDTTADFFLTMTDLSVSTLPLPEVOCFVFNVEYMNCTWNSSEPO 60

QY 61 TNLTLHWYKNSDNDKVKQCSHYLFSEETSGCQKQKEIHLIYQTFVVOLODPREPRQA 120
 DB 61 TNLTLHWYKNSDNDKVKQCSHYLFSEETSGCQKQKEIHLIYQTFVVOLODPREPRQA 120

QY 121 TOMLKLQNLVLPWAPENLTLLKLSQLELNWNNRFLNHLVQYRTDWDHSWTEQSV 180
 DB 121 TOMLKLQNLVLPWAPENLTLLKLSQLELNWNNRFLNHLVQYRTDWDHSWTEQSV 180

QY 181 DYRHKPSLPSVDGQKRYTFRVRSRFPNPLCGSAQHWSESHPIHWSNTSKEN 232
 DB 181 DYRHKPSLPSVDGQKRYTFRVRSRFPNPLCGSAQHWSESHPIHWSNTSKEN 232

RESULT 2
 ABR61610
 ID ABR61610 standard; peptide; 341 AA.
 XX
 AC ABR61610;
 DT 15-JAN-2004 (first entry)
 DE IL-2 common gamma chain (cgammac) fragment (residues 1-341).
 XX
 KW IL-2; interleukin 2; common gamma chain; cgammac; antiinflammatory;
 KW gastrointestinal; antiarthritic; antirheumatic; osteopathic; cardiac;
 KW antisthmatic; noctropic; neuroprotective; antiarteriosclerotic;
 KW immunosuppressive; antithyroid; nuclear factor KB inducing kinase; NIK;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO2003087374-A1.
 PD 23-OCT-2003.
 XX
 PF 15-APR-2003; 2003WO-IL000316.
 XX
 PR 18-APR-2002; 2002IL-00149217.
 PR 08-OCT-2002; 2002IL-00152183.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Wallach D, Ramakrishnan P, Shmushkovich T;
 XX
 DR WPI; 2003-8453330/78.
 XX
 PT New interleukin-2 common gamma chain or its mutein, variant, fusion
 PT protein, functional derivative, circularly permuted derivative or
 PT fragment useful for treating Alzheimer's disease or atherosclerosis.
 XX
 PS Claim 6; Page 97-98; Opp; English.
 XX
 CC The invention relates to an interleukin 2 (IL-2) common gamma chain
 CC (cgammac) or its mutein, variant, fusion protein, functional derivative,
 CC circularly permuted derivative or fragment. Specific antibodies and

CC small molecules capable of modulating the interaction between IL-2
 CC cgammac and nuclear factor KB inducing kinase (NIK) are useful for the
 CC manufacture of a medicament for the treatment of a disease, e.g. a
 CC disease resulting from excessive immune response such as rheumatoid
 CC arthritis, osteoarthritis, inflammatory bowel disease, asthma, cardiac
 CC infarct, Alzheimer's disease or atherosclerosis; or an autoimmune disease
 CC such as immune thyroiditis, or other arthropathies, e.g. autoimmune
 CC haemolytic anemia. The small molecule is useful for modulating signaling
 CC through cgammac. The present sequence represents an IL-2 cgammac protein
 XX
 SQ Sequence 341 AA;

Query Match 100.0%; Score 1288; DB 7; Length 341;
 Best Local Similarity 100.0%; Pred. No. 5.2e-115;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTILTPNGNEDTTADFFLTMTDLSVSTLPLPEVOCFVFNVEYMNCTWNSSEPO 60
 DB 23 LNTTILTPNGNEDTTADFFLTMTDLSVSTLPLPEVOCFVFNVEYMNCTWNSSEPO 82

QY 61 TNLTLHWYKNSDNDKVKQCSHYLFSEETSGCQKQKEIHLIYQTFVVOLODPREPRQA 120
 DB 83 TNLTLHWYKNSDNDKVKQCSHYLFSEETSGCQKQKEIHLIYQTFVVOLODPREPRQA 142

QY 121 TOMLKLQNLVLPWAPENLTLLKLSQLELNWNNRFLNHLVQYRTDWDHSWTEQSV 180
 DB 143 TOMLKLQNLVLPWAPENLTLLKLSQLELNWNNRFLNHLVQYRTDWDHSWTEQSV 202

QY 181 DYRHKPSLPSVDGQKRYTFRVRSRFPNPLCGSAQHWSESHPIHWSNTSKEN 232
 DB 203 DYRHKPSLPSVDGQKRYTFRVRSRFPNPLCGSAQHWSESHPIHWSNTSKEN 254

RESULT 3
 AAR47149
 ID AAR47149 standard; protein; 347 AA.
 XX
 AC AAR47149;
 DT 25-MAR-2003 (revised)
 DT 13-JUN-1994 (first entry)
 XX
 DB IL-2 receptor gamma chain.
 XX
 KW Interleukin-2 receptor gamma chain; IL-2; receptor; immunoregulator;
 KW rheumatoid arthritis; transplant rejection; primer;
 KW polymerase chain reaction; PCR; amplification.
 XX
 OS Homo sapiens.
 XX
 PN EP578932-A2.
 PD 19-JAN-1994.
 XX
 PF 22-APR-1993; 93EP-00106561.
 XX
 PR 23-APR-1992; 92JP-00104947.
 XX
 PA (AJIN) AJINOMOTO KK.
 PA (SUGA) SUGAMURA K.
 XX
 PI Sugamura K, Takeshita T, Asao H, Nakamura M, Shimamura T;
 PI Suzuki M, Hamuro J;
 XX
 DR WPI; 1994-017546/03.
 DR N-PSDB; AAQ54829.
 XX
 PT DNA and protein sequences of IL-2 gamma chain - useful as immune
 PT regulatory agents for treatment of e.g. rheumatoid arthritis and
 PT transplant rejection.
 XX
 PS Claim 4; Page 41; 50pp; English.

XX The human IL-2 receptor gamma chain preform (AAR47148), including the
 CC signal peptide, is encoded by the sequence given in AAQ54828. The mature
 CC protein (AAR47149) is encoded by sequence AAQ54829. A soluble form of IL-
 CC 2 receptor gamma chain (AAR47150) is encoded by AAQ54830, while a soluble
 CC form suitable for expression in prokaryotes (AAR47151) is encoded by
 CC AAQ54831. Primers 1-6 (AAQ54820-25) are based on the N-terminal sequence
 CC of IL-2 receptor gamma chain, and are used to isolate IL2 receptor gamma
 CC chain receptor cDNA. Primers AAQ54826-27 are used to obtain the protein
 CC given in AAR47151. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 347 AA;

Query Match 100.0%; Score 1288; DB 2; Length 347;
 Best Local Similarity 100.0%; Pred. No. 5.3e-115;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVOCFVFNVEYMNCTWNSSEPOP 60
 DB 1 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVOCFVFNVEYMNCTWNSSEPOP 60
 QY 61 TNLTHYWKNSNDKVKQCSHYLFSEETSGCQKKEIHLVQTFVVLQDPREPRQA 120
 DB 61 TNLTHYWKNSNDKVKQCSHYLFSEETSGCQKKEIHLVQTFVVLQDPREPRQA 120
 QY 121 TOMLKLQNLVWPAPENLTLHLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHSHWTEQSV 180
 DB 121 TOMLKLQNLVWPAPENLTLHLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHSHWTEQSV 180
 QY 181 DYRHKPSLPSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHMGNTSKEN 232
 DB 181 DYRHKPSLPSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHMGNTSKEN 232

RESULT 4
 ABR61609
 ID ABR61609 standard; peptide; 357 AA.
 AC ABR61609;
 XX
 DT 15-JAN-2004 (first entry)
 DE IL-2 common gamma chain (cgammac) fragment (residues 1-357).
 XX
 KW IL-2; interleukin 2; common gamma chain; cgammac; antiinflammatory;
 KW gastrointestinal; antiarthritic; antirheumatic; osteopathic; cardiant;
 KW antiasthmatic; nootropic; neuroprotective; antiarteriosclerotic;
 KW immunosuppressive; antithyroid; nuclear factor KB inducing kinase; NIK;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO2003087374-A1.
 XX
 PD 23-OCT-2003.
 XX
 PF 15-APR-2003; 2003WO-IL000316.
 XX
 PR 18-APR-2002; 2002IL-00149217.
 PR 08-OCT-2002; 2002IL-00152183.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX

PI Wallach D, Ramakrishnan P, Shmushkovich T;
 DR WPI; 2003-845330/78.
 XX
 PT New interleukin-2 common gamma chain or its mutein, variant, fusion
 PT protein, functional derivative, circularly permuted derivative or
 PT fragment useful for treating Alzheimer's disease or atherosclerosis.
 XX
 PS Claim 5; Page 96-97; Opp: English.
 XX

CC The invention relates to an interleukin 2 (IL-2) common gamma chain
 CC (cgammac) or its mutein, variant, fusion protein, functional derivative,
 CC circularly permuted derivative or fragment. Specific antibodies and
 CC small molecules capable of modulating the interaction between IL-2
 CC cgammac and nuclear factor KB inducing kinase (NIK) are useful for the
 CC manufacture of a medicament for the treatment of a disease, e.g. a
 CC disease resulting from excessive immune response such as rheumatoid
 CC arthritis, osteoarthritis, inflammatory bowel disease, asthma, cardiac
 CC infarct, Alzheimer's disease or atherosclerosis; or an autoimmune disease
 CC such as immune thyroiditis, or other arthropathies, e.g. autoimmune
 CC haemolytic anemia. The small molecule is useful for modulating signaling
 CC through cgammac. The present sequence represents an IL-2 cgammac protein
 CC fragment
 XX
 SQ Sequence 357 AA;

Query Match 100.0%; Score 1288; DB 7; Length 357;
 Best Local Similarity 100.0%; Pred. No. 5.5e-115;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVOCFVFNVEYMNCTWNSSEPOP 60
 DB 23 LNTTILTPNGNEDTTADFFLTMTPTDLSVSTLPLPEVOCFVFNVEYMNCTWNSSEPOP 82
 QY 61 TNLTHYWKNSNDKVKQCSHYLFSEETSGCQKKEIHLVQTFVVLQDPREPRQA 120
 DB 83 TNLTHYWKNSNDKVKQCSHYLFSEETSGCQKKEIHLVQTFVVLQDPREPRQA 142
 QY 121 TOMLKLQNLVWPAPENLTLHLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHSHWTEQSV 180
 DB 143 TOMLKLQNLVWPAPENLTLHLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHSHWTEQSV 202
 QY 181 DYRHKPSLPSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHMGNTSKEN 232
 DB 203 DYRHKPSLPSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHMGNTSKEN 254

RESULT 5
 AAE13734
 ID AAE13734 standard; protein; 360 AA.
 AC AAE13734;
 XX
 DT 26-FEB-2002 (first entry)
 DE Human soluble IL-2gamma/kappa light chain chimeric DNA construct.
 XX
 KW Human; Zalphall; cytokine receptor; immunosuppressive; cytostatic;
 KW inflammatory disorder; haemostatic; cell proliferation; immune disorder;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
 KW myasthenia gravis; systemic lupus erythematosus; SLE; diabetes; asthma;
 KW ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis;
 KW viral infection; fusion protein; IL-2gamma.
 XX
 OS Homo sapiens.
 XX
 PN WO20017171-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 03-APR-2001; 2001WO-US010872.
 XX
 PR 05-APR-2000; 2000US-0194731P.
 PR 28-JUL-2000; 2000US-0222121P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX

PI Sprecher CA, Novak JE, West JW, Presnell SR, Holly RD, Nelson AJ;
 XX WPI; 2002-025898/03.
 DR N-PSDB; AAD22926.
 XX
 PT Novel soluble receptor polypeptides and polynucleotides used as cytokine

PT antagonist for stimulating ligand activity-induced proliferation of
 XX hematopoietic cells and for suppressing immune response in a mammal.
 PS Example 28; Page 196-197; 243pp; English.
 XX The invention relates to an isolated soluble zalphal1 cytokine receptor
 CC polypeptide and their cDNA molecules. Zalphal proteins are useful for
 CC inhibiting or antagonising the ligand activity-induced proliferation of
 CC haematopoietic cells and haematopoietic cell progenitors preferably
 CC lymphoid cells which are natural killer cells or cytotoxic T cells.
 CC Zalphal is useful for treating immune and inflammatory disorders, for
 CC reducing proliferation of neoplastic B or T cells, for suppressing an
 CC immune response in a mammal exposed to an antigen or pathogen. Zalphal is
 CC useful for treating diseases that require immune regulation including
 CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
 CC myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes;
 CC asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease,
 CC sepsis, viral infection (dengue virus infection) and cancer. The present
 CC sequence is human soluble IL-2Rgamma/kappa light chain fusion protein
 CC construct
 XX Sequence 360 AA;
 SQ Query Match 100.0%; Score 1288; DB 5; Length 360;
 Best Local Similarity 100.0%; Pred. No. 5.6e-115; Mismatches 0; Gaps 0;
 Matches 232; Conservative 0; Indels 0; Gaps 0;
 QY 1 LNTTILTPNGNEDTTADFLTTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPOP 60
 DB 23 LNTTILTPNGNEDTTADFLTTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPOP 82
 QY 61 TNLTLHWYKNSDNDKVKQCSHYLFSEETSGCOLQKKEIHLIYQTFVVLQDPREPRQA 120
 DB 83 TNLTLHWYKNSDNDKVKQCSHYLFSEETSGCOLQKKEIHLIYQTFVVLQDPREPRQA 142
 QY 121 TQMLKLNLIWIPAPENLTLHLKLSQLELNWNNRFLNHLCHLEHLVQYRTDWDHSTEQSV 180
 DB 143 TQMLKLNLIWIPAPENLTLHLKLSQLELNWNNRFLNHLCHLEHLVQYRTDWDHSTEQSV 202
 QY 181 DYRHKFSLPVDGQKRYTFRVSRFNPFCGSAQHSWSESHPIHWGNTSKEN 232
 DB 203 DYRHKFSLPVDGQKRYTFRVSRFNPFCGSAQHSWSESHPIHWGNTSKEN 254
 RESULT 6
 ID AAR47148
 XX AAR47148 standard; protein; 369 AA.
 AC AAR47148;
 XX
 DT 25-MAR-2003 (revised)
 DT 13-JUN-1994 (first entry)
 XX
 XX IL-2 receptor gamma chain.
 XX
 KW Interleukin-2 receptor gamma chain; IL-2; receptor; immunoregulator;
 KW rheumatoid arthritis; transplant rejection; primer; PCR;
 KW polymerase chain reaction; amplification; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX Peptide 1..22
 XX /label= Sig_peptide
 XX
 XX EF578932-A2.
 XX
 XX 19-JAN-1994.
 XX
 XX 22-APR-1993; 93EP-00106561.
 XX
 XX 23-APR-1992; 92JP-00104947.
 XX

PA (AJIN) AJINOMOTO KK.
 XX (SUGA/) SUGAMURA K.
 PI Sugamura K, Takeshita T, Asao H, Nakamura M, Shimamura T;
 PI Suzuki M, Hamuro J;
 DR WPI; 1994-017546/03.
 XX N-PSDB; AAQ54828.
 DR DNA and protein sequences of IL-2 gamma chain - useful as immune
 PT regulatory agents for treatment of e.g. rheumatoid arthritis and
 PT transplant rejection.
 XX
 XX Disclosure; Page 16-17, 29-30; 50pp; English.
 XX The human IL-2 receptor gamma chain preform (AAR47148), including the
 CC signal peptide, is encoded by the sequence given in AAQ54828. The mature
 CC protein (AAR47149) is encoded by sequence AAQ54829. A soluble form of IL-
 CC 2 receptor gamma chain (AAR47150) is encoded by AAQ54830, while a soluble
 CC form suitable for expression in prokaryotes (AAR47151) is encoded by
 CC AAQ54831. Primers 1-6 (AAQ54820-25) are based on the N- terminal sequence
 CC of IL-2 receptor gamma chain, and are used to isolate IL2 receptor gamma
 CC chain receptor cDNA. Primers AAQ54826-27 are used to obtain the protein
 CC given in AAR47151. (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 369 AA;
 SQ Query Match 100.0%; Score 1288; DB 2; Length 369;
 Best Local Similarity 100.0%; Pred. No. 5.8e-115;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNTTILTPNGNEDTTADFLTTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPOP 60
 DB 23 LNTTILTPNGNEDTTADFLTTMTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPOP 82
 QY 61 TNLTLHWYKNSDNDKVKQCSHYLFSEETSGCOLQKKEIHLIYQTFVVLQDPREPRQA 120
 DB 83 TNLTLHWYKNSDNDKVKQCSHYLFSEETSGCOLQKKEIHLIYQTFVVLQDPREPRQA 142
 QY 121 TQMLKLNLIWIPAPENLTLHLKLSQLELNWNNRFLNHLCHLEHLVQYRTDWDHSTEQSV 180
 DB 143 TQMLKLNLIWIPAPENLTLHLKLSQLELNWNNRFLNHLCHLEHLVQYRTDWDHSTEQSV 202
 QY 181 DYRHKFSLPVDGQKRYTFRVSRFNPFCGSAQHSWSESHPIHWGNTSKEN 232
 DB 203 DYRHKFSLPVDGQKRYTFRVSRFNPFCGSAQHSWSESHPIHWGNTSKEN 254
 RESULT 7
 ID AAU96932
 XX AAU96932 standard; protein; 369 AA.
 AC AAU96932;
 XX
 DT 13-AUG-2002 (first entry)
 XX
 XX Human cytokine receptor common gamma chain.
 DE
 DE JAK3; cytostatic; immunomodulatory; antiinflammatory; graft rejection;
 KW human; antirheumatic; infection; hypogammaglobulinaemia; SCID;
 KW severe Combined immunodeficiency; Janus kinase; inflammation;
 KW rheumatoid arthritis; autoimmunity; gamma chain.
 XX
 OS Homo sapiens.
 XX
 XX US6372898-B1.
 XX
 XX 16-APR-2002.
 PD
 XX 13-NOV-1998; 98US-00191786.
 PF
 XX 13-NOV-1998; 98US-00191786.
 PR

XX AC ABU03613;
XX DT 29-JAN-2003 (first entry)
XX DE Human expressed protein tag (EPT) #279.
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX KW protease; protease inhibitor; transporter; cytoskeletal protein;
XX KW receptor; transcription factor; cancer; MHC;
XX KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX FN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOS INC.
XX PI Chicx RM, Tomlinson AJ, Urban RG;
XX DR WPI; 2003-040607/03.
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX PT cytoskeletal proteins, receptors or transcription factors), useful for
XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX PT leukemia.
XX PS Example 2; SEQ ID NO 279; 134pp; English.
XX CC The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor. The
XX CC polypeptide is useful as an immunogenic composition for eliciting in a
XX CC mammal an immunogenic response directed against any of the purified
XX CC polypeptide. The purified polypeptide, or the antibody that binds to this
XX CC polypeptide, is useful for treating cancer. The polypeptide is also
XX CC useful for identifying compounds that binds to a naturally processed
XX CC class I or class II MHC-binding polypeptide. The polypeptides and
XX CC polynucleotides are particularly useful for treating or preventing
XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC lymphoma or leukaemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an
XX CC expressed protein tag (EPT) isolated from human tissue for translational
XX CC profiling. Note: This sequence does not appear in the printed
XX CC specification but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 369 AA;
Query Match 100.0%; Score 1288; DB 6; Length 369;
Best Local Similarity 100.0%; Pred. No. 5.8e-115;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNTLTLPNGNEDTADFFLTMTPTDLSVSLPLPEVQCFVNFVYMNCTWNSSEPOQ 60
DB 23 LNTLTLPNGNEDTADFFLTMTPTDLSVSLPLPEVQCFVNFVYMNCTWNSSEPOQ 82
QY 61 TNLTLHWYKNSDNDKVKQKSHVLFSEETISGQLOKKEIHLVQYFVVLQDPRPRQQA 120
DB 83 TNLTLHWYKNSDNDKVKQKSHVLFSEETISGQLOKKEIHLVQYFVVLQDPRPRQQA 142

QY 121 TOMLKLQNLVLPWAPENLTLLKLSQLELNWNRFLNHLVQYRTDWDHSWTQSV 180
DB 143 TOMLKLQNLVLPWAPENLTLLKLSQLELNWNRFLNHLVQYRTDWDHSWTQSV 202
QY 181 DYRHKFSLPSVDGQKRYTFRVRSRFPNPLCGSAQHWSEWSPHIGSNTSKEN 232
DB 203 DYRHKFSLPSVDGQKRYTFRVRSRFPNPLCGSAQHWSEWSPHIGSNTSKEN 254
RESULT 10
ABU03602
ID ABU03602 standard; protein; 369 AA.
XX AC ABU03602;
XX DT 29-JAN-2003 (first entry)
XX DE Human expressed protein tag (EPT) #268.
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX KW protease; protease inhibitor; transporter; cytoskeletal protein;
XX KW receptor; transcription factor; cancer; MHC;
XX KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX FN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOS INC.
XX PI Chicx RM, Tomlinson AJ, Urban RG;
XX DR WPI; 2003-040607/03.
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX PT cytoskeletal proteins, receptors or transcription factors), useful for
XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX PT leukemia.
XX PS Example 2; SEQ ID NO 268; 134pp; English.
XX CC The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor. The
XX CC polypeptide is useful as an immunogenic composition for eliciting in a
XX CC mammal an immunogenic response directed against any of the purified
XX CC polypeptide. The purified polypeptide, or the antibody that binds to this
XX CC polypeptide, is useful for treating cancer. The polypeptide is also
XX CC useful for identifying compounds that binds to a naturally processed
XX CC class I or class II MHC-binding polypeptide. The polypeptides and
XX CC polynucleotides are particularly useful for treating or preventing
XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC lymphoma or leukaemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an
XX CC expressed protein tag (EPT) isolated from human tissue for translational
XX CC profiling. Note: This sequence does not appear in the printed
XX CC specification but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 369 AA;

Query Match 100.0%; Score 1288; DB 6; Length 369;
 Best Local Similarity 100.0%; Pred. No. 5.8e-115;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTLTITPENGEDTTADFLTTMTPTDSLSVSTLPLPEVQCFVFNVMNCWTNSSSEPPQ 60
 DB 23 LNTLTITPENGEDTTADFLTTMTPTDSLSVSTLPLPEVQCFVFNVMNCWTNSSSEPPQ 82
 QY 61 TNLTLHYWYKNSDNDKVKQKSHYLFSEBITSGCOLQKKEIHLVQYTFVVLQDPREPRQA 120
 DB 83 TNLTLHYWYKNSDNDKVKQKSHYLFSEBITSGCOLQKKEIHLVQYTFVVLQDPREPRQA 142
 QY 121 TQMLKQLNLVWPAPENLTLLKLSQSLELNNRFLNHCLEHLVQYRTDWDHSHWTQSV 180
 DB 143 TQMLKQLNLVWPAPENLTLLKLSQSLELNNRFLNHCLEHLVQYRTDWDHSHWTQSV 202
 QY 181 DYRHKFSPLSDVGQKRYTFRVRSRFPNPLCGSAQHWSEWSHP IHGWSNTSKEN 232
 DB 203 DYRHKFSPLSDVGQKRYTFRVRSRFPNPLCGSAQHWSEWSHP IHGWSNTSKEN 254

RESULT 11
 ABU03603
 ID ABU03603 standard; protein; 369 AA.
 AC ABU03603;
 XX
 DT 29-JAN-2003 (first entry)
 DE Human expressed protein tag (EPT) #269.
 XX
 KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 28-MAR-2002; 2002WO-US009671.
 XX
 PR 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX
 PI Chiciz RM, Tomlinson AJ, Urban RG;
 XX
 DR WPI; 2003-040607/03.
 XX
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 269; 134pp; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting a
 CC mammalian immunogenic response directed against any of the purified
 CC polypeptides. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed

CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 369 AA;

Query Match 100.0%; Score 1288; DB 6; Length 369;
 Best Local Similarity 100.0%; Pred. No. 5.8e-115;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTLTITPENGEDTTADFLTTMTPTDSLSVSTLPLPEVQCFVFNVMNCWTNSSSEPPQ 60
 DB 23 LNTLTITPENGEDTTADFLTTMTPTDSLSVSTLPLPEVQCFVFNVMNCWTNSSSEPPQ 82
 QY 61 TNLTLHYWYKNSDNDKVKQKSHYLFSEBITSGCOLQKKEIHLVQYTFVVLQDPREPRQA 120
 DB 83 TNLTLHYWYKNSDNDKVKQKSHYLFSEBITSGCOLQKKEIHLVQYTFVVLQDPREPRQA 142
 QY 121 TQMLKQLNLVWPAPENLTLLKLSQSLELNNRFLNHCLEHLVQYRTDWDHSHWTQSV 180
 DB 143 TQMLKQLNLVWPAPENLTLLKLSQSLELNNRFLNHCLEHLVQYRTDWDHSHWTQSV 202
 QY 181 DYRHKFSPLSDVGQKRYTFRVRSRFPNPLCGSAQHWSEWSHP IHGWSNTSKEN 232
 DB 203 DYRHKFSPLSDVGQKRYTFRVRSRFPNPLCGSAQHWSEWSHP IHGWSNTSKEN 254

RESULT 12
 ABU03605
 ID ABU03605 standard; protein; 369 AA.
 XX AC ABU03605;
 XX
 DT 29-JAN-2003 (first entry)
 DE Human expressed protein tag (EPT) #271.
 XX
 KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 28-MAR-2002; 2002WO-US009671.
 XX
 PR 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX
 PI Chiciz RM, Tomlinson AJ, Urban RG;
 XX
 DR WPI; 2003-040607/03.
 XX
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.

PT leukemia.
 XX Example 2; SEQ ID NO 271; 134pp; English.
 XX
 XX The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 369 AA;
 XX
 XX Query Match 100.0%; Score 1288; DB 6; Length 369;
 XX Best Local Similarity 100.0%; Pred. No. 5.8e-115;
 XX Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 LNTTILTPNGNEDTTADFFLTMTPTDSLSVSTLPLPEVQCFFVFNVEYNNCTWNSSEPOP 60
 DB 23 LNTTILTPNGNEDTTADFFLTMTPTDSLSVSTLPLPEVQCFFVFNVEYNNCTWNSSEPOP 82
 QY 61 TNLTLHYWYKNSDNDKVKQKSHYLFSEETISGCLQKKEIHLVQYTFVVOLODPREPRQA 120
 DB 83 TNLTLHYWYKNSDNDKVKQKSHYLFSEETISGCLQKKEIHLVQYTFVVOLODPREPRQA 142
 QY 121 TQMLKQLNVLIPWAPENLTLHLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 180
 DB 143 TQMLKQLNVLIPWAPENLTLHLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 202
 QY 181 DYRHKFSLPVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHIGSNTSKEN 232
 DB 203 DYRHKFSLPVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHIGSNTSKEN 254
 XX
 XX RESULT 13
 XX ABU03600
 XX ID ABU03600 standard; protein; 369 AA.
 XX AC ABU03600;
 XX XX
 XX 29-JAN-2003 (first entry)
 XX Human expressed protein tag (EPT) #266.
 XX
 XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX
 XX Homo sapiens.
 XX
 XX W0200278524-A2.
 XX
 XX 10-OCT-2002.
 XX
 XX 28-MAR-2002; 2002W0-US009671.
 XX
 XX 28-MAR-2001; 2001US-0279495P.
 XX 21-MAY-2001; 2001US-0252544P.
 XX 08-AUG-2001; 2001US-0310801P.
 XX 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 XX (ZYCO-) ZYCOS INC.
 XX
 XX Chicz RM, Tomlinson AJ, Urban RG;
 XX WPI; 2003-040607/03.
 XX
 XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 XX Example 2; SEQ ID NO 266; 134pp; English.
 XX
 XX The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 369 AA;
 XX
 XX Query Match 100.0%; Score 1288; DB 6; Length 369;
 XX Best Local Similarity 100.0%; Pred. No. 5.8e-115;
 XX Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 LNTTILTPNGNEDTTADFFLTMTPTDSLSVSTLPLPEVQCFFVFNVEYNNCTWNSSEPOP 60
 DB 23 LNTTILTPNGNEDTTADFFLTMTPTDSLSVSTLPLPEVQCFFVFNVEYNNCTWNSSEPOP 82
 QY 61 TNLTLHYWYKNSDNDKVKQKSHYLFSEETISGCLQKKEIHLVQYTFVVOLODPREPRQA 120
 DB 83 TNLTLHYWYKNSDNDKVKQKSHYLFSEETISGCLQKKEIHLVQYTFVVOLODPREPRQA 142
 QY 121 TQMLKQLNVLIPWAPENLTLHLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 180
 DB 143 TQMLKQLNVLIPWAPENLTLHLKLSQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 202
 QY 181 DYRHKFSLPVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHIGSNTSKEN 232
 DB 203 DYRHKFSLPVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHIGSNTSKEN 254
 XX
 XX RESULT 14
 XX ABU03601
 XX ID ABU03601 standard; protein; 369 AA.
 XX AC ABU03601;
 XX XX
 XX 29-JAN-2003 (first entry)
 XX Human expressed protein tag (EPT) #267.
 XX
 XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

OS Homo sapiens.
FN WO200278524-A2.
PD 10-OCT-2002.
PF 28-MAR-2002; 2002WO-US009671.
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX (ZYCO-) ZYCOS INC.
FA Chicx RM, Tomlinson AJ, Urban RG;
FI WPI; 2003-040607/03.
DR New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 267; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, or protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 369 AA;
Query Match 100.0%; Score 1288; DB 6; Length 369;
Best Local Similarity 100.0%; Pred. No. 5.8e-115; Indels 0; Gaps 0;
Matches 232; Conservative 0; Mismatches 0;
QY 1 LNTLTITPNEGNETTADFFLTMTPTDSLVSSTLPPEVQCFVFNVEYMNCTWNSSESPQP 60
Db 23 LNTLTITPNEGNETTADFFLTMTPTDSLVSSTLPPEVQCFVFNVEYMNCTWNSSESPQP 82
QY 61 TNLTLHYWYKNSDNDKVKQCSHYLFSEBITSGCLOKKEIHLVYTFVQLODPRPRQA 120
Db 83 TNLTLHYWYKNSDNDKVKQCSHYLFSEBITSGCLOKKEIHLVYTFVQLODPRPRQA 142
QY 121 TOMLKLQNLVLPWAPENLTILKLSQLELNWNRFLNHLVQVYRTDWDHSWTESQV 180
Db 143 TOMLKLQNLVLPWAPENLTILKLSQLELNWNRFLNHLVQVYRTDWDHSWTESQV 202
QY 181 DYRHKFLSPVDGQKRYTFRVRSFNPFLCGSAQHSWNSHPHIGWNTSKEN 232
Db 203 DYRHKFLSPVDGQKRYTFRVRSFNPFLCGSAQHSWNSHPHIGWNTSKEN 254
RESULT 15
AAY92202
ID AAY92202 standard; protein; 691 AA.
XX

AC AAY92202;
XX 01-AUG-2000 (first entry)
XX
XX Fusion polypeptide 603, IL-4 trap.
DE IL-4 trap; cytokine; antagonist; CNTF; receptor; fusion protein;
KW cytostatic; immunomodulator; osteopathic.
XX Synthetic.
OS Homo sapiens.
XX WO200018932-A2.
XX 06-APR-2000.
XX 22-SEP-1999; 99WO-US022045.
PF 25-SEP-1998; 98US-0101858P.
PR 19-MAY-1999; 99US-00313942.
XX (REGS-) REGENERON PHARM INC.
PA Stahl N, Yancopoulos GD;
XX WPI; 2000-293165/25.
XX N-PSDB; AAA09044.
DR Isolated nucleic acid molecule for treating cytokine-related diseases or
PT disorders encodes a fusion polypeptide capable of binding a cytokine to
PT form a nonfunctional complex.
XX Example 6; Fig 22A-D; 152pp; English.
XX This sequence shows fusion polypeptide 603, which is capable of binding
CC cytokine IL-4 to form a non-functional complex. The invention concerns
CC production of antagonists to any cytokine that utilizes an alpha
CC specificity determining component, which when combined with the cytokine,
CC binds to a first beta signal transducing component to form a non-
CC functional intermediate which then binds to a second beta signal
CC transducing component causing beta-receptor dimerization, the soluble
CC alpha specificity determining component of the receptor (SR-alpha) and
CC the extracellular domain of the first beta signal transducing component
CC of the cytokine receptor (beta-1) are combined to form heterodimers (SR-
CC alpha:beta-1) that act as antagonist to the cytokine by binding the
CC cytokine to form a non-functional complex. The receptor components are
CC shared by cytokines such as the CNTF (Ciliary neurotrophic factor) family
CC of cytokines. The invention provides the basis for the development of IL-
CC 6 antagonists, as they show that if, in the presence of a ligand, a non-
CC functional intermediate complex, consisting of the ligand, its alpha
CC receptor and its beta-1 receptor component, can be formed, it will
CC effectively block the action of the ligand. Effective antagonists of IL-6
CC or CNTF consist of heterodimers of the extracellular domains of the alpha
CC specificity determining components of their receptors and the
CC extracellular domain of gp130. The resultant heterodimers, function as
CC high-affinity traps, rendering the cytokine inaccessible to form a signal
CC transducing complex with the native membrane-bound forms of their
CC receptor. The nucleic acids and polypeptides are useful for treating
CC cytokine-related diseases or disorders such as osteoporosis and primary
CC and secondary effects of cancer including multiple myeloma or cachexia
XX
SQ Sequence 691 AA;
Query Match 100.0%; Score 1288; DB 3; Length 691;
Best Local Similarity 100.0%; Pred. No. 1.4e-114; Indels 0; Gaps 0;
Matches 232; Conservative 0; Mismatches 0;
QY 1 LNTLTITPNEGNETTADFFLTMTPTDSLVSSTLPPEVQCFVFNVEYMNCTWNSSESPQP 60
Db 23 LNTLTITPNEGNETTADFFLTMTPTDSLVSSTLPPEVQCFVFNVEYMNCTWNSSESPQP 82
QY 61 TNLTLHYWYKNSDNDKVKQCSHYLFSEBITSGCLOKKEIHLVYTFVQLODPRPRQA 120
XX

Db 83 TNLTLHYWKNSDNDKVKCSHYLFSEBITSGCQLQKKEIHLVQTFVVQLQDPREPRQA 142
Qy 121 TOMLKLQNLVIFWAPENLTLHKLSQSLELNNRFLNHCLEHLVQYRTDWDHSHWTQSV 180
Db 143 TOMLKLQNLVIFWAPENLTLHKLSQSLELNNRFLNHCLEHLVQYRTDWDHSHWTQSV 202
Qy 181 DYRHKFSLPSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSKEN 232
Db 203 DYRHKFSLPSVDGQKRYTFRVRSRFPNPLCGSAQHSEWSHPHWSNTSKEN 254

Search completed: March 3, 2004, 12:35:37
Job time : 57.3464 secs

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DM protein - protein search, using sw model

Run on: March 3, 2004, 12:31:14 ; Search time 26.4706 Seconds
(without alignments)

1930.971 Million cell updates/sec

Title: US-09-825-561A-10

Perfect score: 850

Sequence: 1 MRSSPGNMERIVCLMVFL.....LQKMIHQLSRTHGSEDS 162

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 31518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	850	100.0	162	4 Q9HBE4	Q9HBE4 homo sapien
2	486	57.2	146	11 Q9ES17	Q9ES17 mus musculus
3	392	46.1	123	11 Q80XG2	Q80XG2 peromyscus
4	85	10.0	311	5 Q9I913	Q9I913 loxosceles
5	84.5	9.9	722	16 Q8D8P4	Q8D8P4 vibrio vuln
6	83.5	9.8	582	16 Q8DUS6	Q8DUS6 synchococc
7	83.5	9.8	3052	12 Q82933	Q82933 johnsongras
8	83	9.8	899	2 Q82336	Q82336 salmorella
9	83	9.8	899	2 Q9R2J7	Q9R2J7 shigella so
10	83	9.8	1224	16 Q8CPT9	Q8CPT9 staphylococ
11	81.5	9.6	566	5 Q9VY88	Q9VY88 drosophila
12	81	9.5	140	13 Q8JFF4	Q8JFF4 anas platyr
13	81	9.5	163	5 Q966R0	Q966R0 dictyostell
14	81	9.5	385	5 Q9VJL7	Q9VJL7 drosophila
15	81	9.5	414	5 Q9NK60	Q9NK60 drosophila
16	80	9.4	140	13 Q804B7	Q804B7 cairina mos

Q8IK96 plasmodium
Q9W756 gallus gall
Q91Y09 mus musculu
Q80X92 mus musculu
Q8EUW0 mycoplasma
Q8MMA4 drosophila
Q9JJ48 mus musculu
Q7XYP8 oryza sativ
Q9ELI4 homo sapien
Q8WVP0 homo sapien
Q8MYV8 drosophila
Q9VY89 drosophila
Q23239 calliphora
Q9W3H8 drosophila
Q8WRS2 drosophila
Q8WRS3 drosophila
Q9W3H6 drosophila
Q8ERW4 encephalito
Q86IV0 dictyosteli
Q9DEV5 gallus gall
Q9BFF3 didelphis m
Q22975 caenorhabdi
Q8K5L8 streptococc
Q8BLA1 mus musculu
Q86KI1 dictyosteli
Q81RP4 drosophila
Q813M4 plasmodium
Q8IIL9 plasmodium
Q96C15 homo sapien

ALIGNMENTS

RESULT 1

Q9HBE4
ID Q9HBE4 PRELIMINARY; PRT; 162 AA.
AC Q9HBE4;
DT 01-MAR-2001 (TREMREL. 16, Created)
DT 01-MAR-2001 (TREMREL. 16, Last sequence update)
DT 01-JUN-2003 (TREMREL. 24, Last annotation update)
DE Interleukin 21.
GN IL21.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.

RP MEDLINE=2031754; PubMed=11081504;
RX Parrish-Novak J., Dillon S.R., Nelson A., Hammond A., Sprecher C.,
RA Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader S.,
RA Burkhead S., Heibel M., Brandt C., Kuipjer J.L., Kramer J.,
RA Conklin D., Presnell S.R., Berry J., Shiota F., Bort S., Hamby K.,
RA Mudri S., Clegg C., Moore M., Grant F.J., Lofton-Day C., Gilbert T.,
RA Rayond F., Ching A., Yao L., Smith D., Webster P., Whitmore T.,
RA Maurer M., Kaushansky K., Holly R.D., Foster D.,
RT "Interleukin 21 and its receptor are involved in NK cell expansion and
regulation of lymphocyte function."
RL Nature 408:57-63(2000).
DR EMBL; AF254069; AAG29348.1; -
DR Genew; HGNC:6005; IL21.
DR GO; GO:0005634; Cnucleus; NAS
DR GO; GO:0005125; Fcytokine activity; NAS.
DR GO; GO:0007515; P.lymph gland development; NAS.
DR GO; GO:0007165; P.signal transduction; NAS.
SQ SEQUENCE 162 AA; 18652 MW; 54EFD4ED3AB97FE CRC64;

Query Match 100.0%; Score 850; DB 4; Length 162;

Best Local Similarity 100.0%; Pred. No. 8.7e-80;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGNMERIVCLMVFLGLTFLVHKSSQGDHMRQLDIVDOLKNYVNDLVEEF 60

```
Db 1 MRSSGNNRIVICLVIFLGLTVLHKSSSQGDREIMRQLDIVDQLKNYVNDLVPEF 60
Qy 61 LPAPEDVETNCWAFSCFQKQALKSANTGNNEIINVSIKLKRKPPSTNAGRRQKRL 120
Db 61 LPAPEDVETNCWAFSCFQKQALKSANTGNNEIINVSIKLKRKPPSTNAGRRQKRL 120
Qy 121 TCPSCDSYKPPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
Db 121 TCPSCDSYKPPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
RESULT 2
Q9ES17 PRELIMINARY; PRT; 146 AA.
AC Q9ES17;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Interleukin 21.
GN IL21.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BAUS/C;
RX MEDLINE=20531754; PubMed=11081504;
RA Parrish-Novak J., Dillon S.R., Nelson A., Hammond A., Sprecher C.,
RA Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader S.,
RA Burkhead S., Heibel M., Brandt C., Kuljper J.L., Kramer J.,
RA Conklin D., Presnell S.R., Berry J., Shiota F., Bort S., Hamby K.,
RA Mudri S., Clegg C., Moore M., Grant F.J., Lofton-Day C., Gilbert T.,
RA Raymond F., Chang A., Yao L., Smith D., Webster P., Whitmore T.,
RA Maurer M., Kaushansky K., Holly R.D., Foster D.;
RT "Interleukin 21 and its receptor are involved in NK cell expansion and
RT regulation of lymphocyte function.";
RL Nature 408:57-63(2000).
DR EMBL; AF254070; AAG29349.1; -.
DR MGD; MGI:1890474; IL21.
DR GO; GO:0005126; F:hematopoietin/interferon-class (D200-domain. .; IDA.
SQ SEQUENCE 146 AA; 16811 MW; D2527ED958A15194 CRC64;
Query Match 57.2%; Score 486; DB 11; Length 146;
Best Local Similarity 63.0%; Pred. No. 2.9e-42;
Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;
Qy 8 MERIVICLVIFLGLTVLHKSSSQGDREIMRQLDIVDQLKNYVNDLVPEFLPAPDV 67
Db 1 MERTVCLVIFLGLTVLHKSSSQGDREIMRQLDIVDQLKNYVNDLVPEFLPAPDV 60
Qy 68 ETNCWAFSCFQKQALKSANTGNNEIINVSIKLKRKPPSTNAGRRQKRLTCPSCDS 127
Db 61 KGHCHEAFACTQKAKLPSNFKNTFFIDLVQLRRRLPARRGGKQKHLAKPCSCDS 120
Qy 128 YKPPKPEFLERFKSLQKMIHQHLS 153
Db 121 YKRTPEFLERLKWLLQKMIHQHLS 146
RESULT 3
Q80XG2 PRELIMINARY; PRT; 123 AA.
ID Q80XG2
AC Q80XG2;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Interleukin-21 (Fragment).
GN IL21.
OS Peromyscus maniculatus (Deer mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
```

```
OC Peromyscus.
OX NCBI_TaxID=10042;
RN [1]
RP SEQUENCE FROM N.A.
RA Schountz T., Buniger A., Davenport B., Hegg T.;
RT "Cloning of deer mouse IL-2, IL-12 p35, IL-21, GM-CSF, CCL3 and CCL4
RT cDNAs.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY247761; AAP04420.1; -.
FT NON_TER 1
FT NON_TER 123
SQ SEQUENCE 123 AA; 13945 MW; 8656C8EA95447E34 CRC64;
Query Match 46.1%; Score 392; DB 11; Length 123;
Best Local Similarity 60.2%; Pred. No. 1.2e-32;
Matches 74; Conservative 24; Mismatches 25; Indels 0; Gaps 0;
Qy 16 MVIFLGLTVLHKSSSQGDREIMRQLDIVDQLKNYVNDLVPEFLPAPDVETNCWESA 75
Db 1 VVIFLGLTVLHKSSSQGDREIMRQLDIVDQLKNYVNDLVPEFLPAPDVVKHCAHSA 60
Qy 76 FSCFQKQALKSANTGNNEIINVSIKLKRKPPSTNAGRRQKRLTCPSCDSYKPPKPE 135
Db 61 FACFQKALKPANTGSKNTIISDLVTLRRRLPATKAEKQKQSLVKPCDSYKPPKPE 120
Qy 136 FLE 138
Db 121 FLE 123
RESULT 4
Q81913 PRELIMINARY; PRT; 311 AA.
ID Q81913
AC Q81913;
DT 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DB Sphingomyelinase-like protein.
OS Loxosceles laeta.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Haplogynae; Sicariidae; Loxosceles.
OX NCBI_TaxID=58217;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=22306580; PubMed=12419302;
RA Pedrosa M.F.F., Junqueira de Azevedo I.L.M.,
RA Goncalves-de-Andrade R.M., van den Berg C.W., Ramos C.R.R., Ho P.L.,
RA Tambourgi D.V.;
RT "Molecular cloning and expression of a functional dermonecrotic and
RT haemolytic factor from Loxosceles laeta venom.";
RL Biochem. Biophys. Res. Commun. 298:638-645(2002).
DR EMBL; AY093600; AAM21155.1; -.
DR GO; GO:0008889; F:glycerophosphodiester phosphodiesterase act. .; IEA.
DR GO; GO:0006071; P:glycerol metabolism; IEA.
DR InterPro; IPR004129; GDPD.
DR Pfam; PF03009; GDPD; 1.
DR SEQUENCE 311 AA; 35451 MW; 39040EB3A21F56E1 CRC64;
Query Match 10.0%; Score 85; DB 5; Length 311;
Best Local Similarity 23.1%; Pred. No. 1.8;
Matches 42; Conservative 23; Mismatches 71; Indels 46; Gaps 7;
Qy 11 IVICLVIFLGLTVLHKSSSQGDREIMRQLDIVDQLKNYVND-----LV 57
Db 8 ILGCVTVLGAETDVGDERADKERPIWNLGHMVNAVKQIPTFLNDGANAIEADITPKGAV 67
Qy 58 P--EFLPAPDVETNC--EWSAFSCFQK-----OLKSANTGNNE 93
Db 68 PTYSYHGTPCDFGRDCIRWEYDFVLTQRTDTPGNSKYKFKFILFVLDLTKGSLNNNE 127
Qy 94 -RIINYSIKK--LKRKPPSTNAGRRQKRLTCPSCDSYKPPKPEFLERFKSLQKMIHQ 150
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Db 128 VRAGENIAKGLLNKYNWNGNGRAYVLSLDIAHY-----EFIRPKFVLAEGHE 181

Dy 151 HL 152

Dz 182 NL 183

RESULT 5

8D6P4 PRELIMINARY; PRT; 722 AA.

Q8D6P4

AC Q8D6P4; (TREMELrel. 23, Created)

DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)

DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 23, Last annotation update)

DE ABC-type bacteriocin/antibiotic exporters.

DN VV20484.

DS Vibrio vulnificus.

DC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;

CC Vibrionaceae; Vibrio.

DX NCBI_TaxID=672;

DN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CMCP6;

RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,

RA Choy H.E.;

RT "Complete genome sequence of *Vibrio vulnificus* CMCP6.";

RL Submitted (DRC-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE016809; AA007435.1; -

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:000524; F:ATP binding; IEA.

DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. .; IEA.

DR GO; GO:000166; F:nucleotide binding; IEA.

DR GO; GO:0004849; F:uridine kinase activity; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR003593; AAA_ATPase.

DR InterPro; IPR001140; ABC_TM_transport.

DR InterPro; IPR003439; ABC_transporter.

DR Pfam; PF00664; ABC_membrane; 1.

DR Pfam; PF00005; ABC_tran; 1.

DR PRINTS; PR00988; URIDINKINASE.

DR PRODOM; PD000006; ABC_transporter; 1.

DR SMART; SM00382; AAA_1.

DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.

DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.

KW Complete proteome.

SQ SEQUENCE 722 AA; 79857 MW; B8967F3B930C0205 CRC64;

Query Match 9.8%; Score 84.5; DB 16; Length 722;

Best Local Similarity 25.0%; Pred. No. 5.4; Indels 25; Gaps 6;

Matches 36; Conservative 26; Mismatches 57; Indels 25; Gaps 6;

Qy 17 VIFGLTLVHKSSSQQDRHMI-----RMQLIDIVDLQKKNYNDL---VPEFLPA 63

Dz 32 VYAGQPHKKSSSQQLKHALGVSHALSDMEREADYLG-LKSQVTLTQALDTLPL 90

Qy 64 PEDVETNCWAPSCFQXQALKSANTGNNEIIVSIKLLKPKPPSTNAGROKRLTCTP 123

Dz 91 PALIENHGW-----QVITQVSDGHWTFFDPSTQQLQTPVSPNSQR-KHKVMLL 140

Qy 124 SCDSYEKKPKPELRF-KSLQK 146

Dz 141 ADEQLSSKEVKFGLSWFAPSILRQ 164

RESULT 6

Q8DJS6 PRELIMINARY; PRT; 582 AA.

AC Q8DJS6;

DT 01-MAR-2003 (TREMELrel. 23, Created)

DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)

DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)

DE Tlr1146 protein.

GN TLR1146.

OS Synchococcus elongatus (Thermosynechococcus elongatus).

OC Bacteria; Cyanobacteria; Chroococcales; Synchococcus.

OX NCBI_TaxID=32046;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BP-1;

RX MEDLINE=2225144; PubMed=12240834;

RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Kato H., Sasamoto S.,

RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,

RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,

RA Shimpō S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;

RT "Complete genome structure of the thermophilic cyanobacterium

RT Thermosynechococcus elongatus BP-1.";

RL DNA Res. 9,123-130(2002).

RL EMBL; AF005372; BAC08698.1; -

DR GO; GO:0016020; C:membrane; IEA.

DR InterPro; IPR006685; MSion_channel.

DR Pfam; PF00924; MS_channel; 1.

KW Complete proteome.

SQ SEQUENCE 582 AA; 66407 MW; DF0A33E93614A92D CRC64;

Query Match 9.8%; Score 83.5; DB 16; Length 582;

Best Local Similarity 21.6%; Pred. No. 5.4; Indels 21; Gaps 3;

Matches 21; Conservative 24; Mismatches 31; Indels 21; Gaps 3;

Qy 81 KAQLKSANTGNNEIIVSIKLLKPKPPSTNAGROKHE-----LTCP 123

Dz 91 RAELIQSNL---RAVLHSALEADRRSPARVDIGVARLHNLVISARIGQABRTTLLT 147

Qy 124 SCDS-YEKKPKPELRFKSLQKKNHLSRTHGS 159

Dz 148 EADSDYHQLPPETLAQQRDLQEQMNAIQERTHAA 184

RESULT 7

Q82933 PRELIMINARY; PRT; 3052 AA.

AC Q82933;

DT 01-NOV-1996 (TREMELrel. 01, Created)

DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE Viral proteins.

OS Johnsongrass mosaic virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;

OC Potyvirus.

OX NCBI_TaxID=31742;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94200956; PubMed=8150599;

RA Gough K.H., Shukla D.D.;

RT "the nucleotide sequence of Johnson grass mosaic potyvirus genomic

RT RNA.";

RL Intervirology 36:181-192(1993).

RN [2]

RP SEQUENCE FROM N.A.

RA Gough K.H.;

RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Nurhayati E.;

RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.

DR EMBL; Z36920; CAAB1549.1; -

DR MEROPS; C04_011; -

DR MEROPS; C06_001; -

DR MEROPS; S30_001; -

DR GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0008026; F:ATP dependent helicase activity; IEA.

DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.

DR GO; GO:0016787; F:hydrolase activity; IEA.

DR GO; GO:0003676; F:nucleic acid binding; IEA.

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DR GO: GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO: GO:0005128; P:structural molecule activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO: GO:0006350; P:transcription; IEA.
DR GO: GO:0009079; P:viral genome replication; IEA.
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR001650; Helicase C.
DR InterPro: IPR001730; Peptidase C4.
DR InterPro: IPR001456; Peptidase C6.
DR InterPro: IPR001592; Pcty-coat.
DR InterPro: IPR002540; Pcty-Fi.
DR InterPro: IPR007095; RNA_pol_DS_PS.
DR InterPro: IPR001205; RNA_pol_P3D.
DR InterPro: IPR007094; RNA_pol_Psvir.
DR Pfam: PF00271; helicase C; 1.
DR Pfam: PF00863; Peptidase C4; 1.
DR Pfam: PF00851; Peptidase C6; 1.
DR Pfam: PF00767; Pcty-coat; 1.
DR Pfam: PF01577; Pcty-Fi; 1.
DR Pfam: PF00680; RNA_Dep_RNA_pol; 1.
DR PRINTS: PRO00966; NIAPCTPTASE.
DR SMART: SM00487; DEXDc; 1.
DR SMART: SM00490; HELICc; 1.
KW ATP-binding; Coat protein; Helicase; Hydrolase.
FT CHAIN 239 699 HELPER COMPONENT (HC).
FT CHAIN 700 1046 PROTEASE3.
FT CHAIN 1047 1098 6K1.
FT CHAIN 1099 1757 CYTOPLASMIC INCLUSION (CI).
FT CHAIN 1758 1803 6K2.
FT CHAIN 1804 1991 SMALL NUCLEAR INCLUSION/VIRUS ATTACHED PROTEIN.
FT CHAIN 1992 2233 SMALL NUCLEAR INCLUSION/PROTEASE.
FT CHAIN 2234 2749 LARGE NUCLEAR INCLUSION/POLYMERASE.
FT CHAIN 2750 3052 COAT PROTEIN.
SQ SEQUENCE 3052 AA; 347247 MW; 08CD8831A73EBCA9 CRC64;

Query Match 9.8%; Score 83.5; DB 12; Length 3052;
Best Local Similarity 23.1%; Pred. No. 38;
Matches 25; Conservative 23; Mismatches 57; Indels 3; Gaps 3;

OY 45 IVDLQNYNDLVPEFLPAPEDVETNCVSAFCQKALQSANTGNRIINVSIIKLLK 104
Db 220 LVNALDQYED-VKQICHYSFDAEAFKFGTENHTAQREARHDTHPEV-MSEVBCG 277
OY 105 RKPPSTNAGROKHRLTCRSC-DSYEKKPKPEFLERFKSLLOKWIHOH 151
Db 278 RRAAMLENAFHQGFKITCKKCFQTFDEHSDDEVCEIHNALQRIEQN 325

RESULT 8
ID Q52336 PRELIMINARY; PRT; 899 AA.
AC Q52336;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE NIKB protein.
GN NIKB.
OS Salmonella typhimurium.
OC Plasmid R64.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=drd-11; PLASMID=R64;
RX MEDLINE=96198143; PubMed=8626273;
RA Furuya N., Komano T.;
RT "Nucleotide sequence and characterization of the trbABC region of the IncII plasmid R64: existence of the pnd gene for plasmid maintenance within the transfer region.";
RT J. Bacteriol. 178:1491-1497(1996).
RN [2]

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RP SEQUENCE FROM N.A.
RC STRAIN=drd-11; PLASMID=R64;
RX MEDLINE=91177811; PubMed=1848841;
RA Furuya N., Nishioka T., Komano T.;
RT "Nucleotide sequence and functions of the orit operon in IncII plasmid R64.";
RL J. Bacteriol. 173:2231-2237(1991).
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN=drd-11; PLASMID=R64;
RA Komano T., Narahara K., Yoshida T., Furuya N.;
RT "The transfer region of IncII plasmid R64: similarities between R64 tra genes and Legionella lcn/dot genes.";
RN Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A.
RC STRAIN=drd-11; PLASMID=R64;
RX MEDLINE=92011438; PubMed=1917882;
RA Furuya N., Komano T.;
RT "Determination of the nick site at orit of IncII plasmid R64: global similarity of orit structures of IncII and IncP plasmids.";
RL J. Bacteriol. 173:6612-6617(1991).
RN [5]
RN SEQUENCE FROM N.A.
RC STRAIN=drd-11; PLASMID=R64;
RX MEDLINE=98053841; PubMed=9393692;
RA Furuya N., Komano T.;
RT "Mutational analysis of the R64 orit region: requirement for precise location of the Nika-binding sequence.";
RL J. Bacteriol. 179:7291-7297(1997).
RN [6]
RN SEQUENCE FROM N.A.
RC STRAIN=drd-11; PLASMID=R64;
RX MEDLINE=98268996; PubMed=9603870;
RA Yoshida T., Furuya N., Ishikura M., Isobe T., Haino-Fukushima K., Ogawa T., Komano T.;
RT "Purification and characterization of thin pili of IncII plasmids Colib-P9 and R64: formation of Pili-specific cell aggregates by type IV pili.";
RL J. Bacteriol. 180:2842-2848(1998).
RN [7]
RN SEQUENCE FROM N.A.
RC STRAIN=drd-11; PLASMID=R64;
RX MEDLINE=94132048; PubMed=8300611;
RA Pansegrau W., Schroder W., Lanka E.;
RT "Concerted action of three distinct domains in the DNA cleaving-joining reaction catalyzed by relaxase (TraI) of conjugative plasmid RP4.";
RL J. Biol. Chem. 269:2782-2789(1994).
RN [8]
RN SEQUENCE FROM N.A.
RC STRAIN=drd-11; PLASMID=R64;
RX MEDLINE=94285211; PubMed=8014987;
RA Pansegrau W., Lanka E., Barth P.T., Figurski D.H., Guiney D.G., Haas D., Helinski D.R., Schwab H., Stanisich V.A., Thomas C.M.;
RT "Complete nucleotide sequence of Birmingham IncP-alpha plasmids: compilation and comparative analysis.";
RL J. Mol. Biol. 239:623-663(1994).
RN [9]
RN SEQUENCE FROM N.A.
RC PLASMID=R64;
RA Saepi G., Komano T., Sasaki T., Tachibana K., Furuya N., Saito Y., Suzuki T., Mizobuchi K.;
RT "Organization and diversification of plasmid genomes: complete nucleotide sequence of R64 genome.";
RN Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [10]
RN SEQUENCE FROM N.A.
RC PLASMID=R64;
RX MEDLINE=87145423; PubMed=3029698;
RA Komano T., Kubo A., Nishioka T.;
RT "Shufflon: multi-inversion of four contiguous DNA segments of plasmid R64 creates seven different open reading frames.";
RN

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RL Nucleic Acids Res. 15:1165-1172(1987).
 RN [11]
 RP SEQUENCE FROM N.A.
 RC PLASMID=R64;
 RX MEDLINE=89127142; PubMed=3065610;
 RA Kubo A., Kusukawa A., Komano T.;
 RT "Nucleotide sequence of the rsi gene encoding shufflon-specific DNA
 recombination in the IncII plasmid R64: homology to the site-specific
 recombination of integrase family";
 RL Mol. Gen. Genet. 213:30-35(1988).
 RN [12]
 RP SEQUENCE FROM N.A.
 RC PLASMID=R64;
 RX MEDLINE=88314948; PubMed=3045094;
 RA Komano T., Toyoshima A., Morita K., Nishioka T.;
 RT "Cloning and nucleotide sequence of the oriI region of the IncII
 plasmid R64";
 RL J. Bacteriol. 170:4385-4387(1988).
 RN [13]
 RP SEQUENCE FROM N.A.
 RC PLASMID=R64;
 RX MEDLINE=93352408; PubMed=8349545;
 RA Kim S.R., Funayama N., Komano T.;
 RT "Nucleotide sequence and characterization of the traABCD region of
 IncII plasmid R64";
 RL J. Bacteriol. 175:5035-5042(1993).
 RN [14]
 RP SEQUENCE FROM N.A.
 RC PLASMID=R64;
 RX MEDLINE=95083745; PubMed=7991676;
 RA Furuya N., Komano T.;
 RT "Surface exclusion gene of IncII plasmid R64: nucleotide sequence and
 analysis of deletion mutants";
 RL Plasmid 32:80-84(1994).
 RN [15]
 RP SEQUENCE FROM N.A.
 RC PLASMID=R64;
 RX MEDLINE=97428559; PubMed=9281491;
 RA Narahara K., Rahman E., Furuya N., Komano T.;
 RT "Requirement of a limited segment of the sog gene for plasmid R64
 conjugation";
 RL Plasmid 38:1-11(1997).
 RN [16]
 RP SEQUENCE FROM N.A.
 RC PLASMID=R64;
 RX MEDLINE=97315231; PubMed=9171405;
 RA Kim S.R., Komano T.;
 RT "The plasmid R64 thin pilus identified as a type IV pilus";
 RL J. Bacteriol. 179:3594-3603(1997).
 RN [17]
 RP SEQUENCE FROM N.A.
 RC PLASMID=R64;
 RX MEDLINE=20223621; PubMed=10760136;
 RA Komano T., Yoshida T., Narahara K., Furuya N.;
 RT "The transfer region of IncII plasmid R64: similarities between R64
 tra genes and Legionella icm/dot genes";
 RL Mol. Microbiol. 35:1348-1359(2000).
 DR EMBL; AB027308; BAB78021.1; -;
 DR EMBL; AF005147; BAB91644.1; -;
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 DR InterPro; IPR005094; Relaxase.
 DR Pfam; PF03432; Relaxase; 1.
 KW Plasmid.
 SQ SEQUENCE 899 AA; 104010 MW; C062A360B275C337 CRC64;

Query Match 9.8%; Score 83; DB 2; Length 899;
 Best Local Similarity 22.5%; Pred. No. 10;
 Matches 34; Conservative 22; Mismatches 55; Indels 40; Gaps 7;

QY 27 SSSQCDRHMTMROLIIVOLKNYNDLVPPELPAPEDVETNCWSAF---SCFQKAQ 83
 DB 38 SSSQAEQPHRSRSLVDYATRLRN-----ESFVALVDVMKDCGEWVNFVGTVCFNCT 91
 QY 84 LKSANTGNNERIINVSIIKLRKPPSTNAGRRQKRL---TCP-----SCDSYKPKPK 134
 DB 92 SLETAADMEYI-----ARQAHYAKDDTDPVHYILSWQSHSPRPE 133
 QY 135 EFLERFKSLLOKM---IHQHLSSRTHGSEDS 162
 DB 134 QIYDSVRHTLKSGLADHQYVSA-VHTDTDN 163

RESULT 9
 Q9R2J7 PRELIMINARY; PRT; 899 AA.
 AC Q9R2J7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Relaxase.
 GN NIKB.
 OS Shigella sonnei.
 OG Plasmid Col1b-P9.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Shigella.
 OX NCBI_TaxID=624;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=P9;
 RA Sampei G., Mizobuchi K.;
 RT "Organization and diversification of plasmid genomes: complete
 nucleotide sequence of the Col1b-P9 genome";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB021078; BAA75140.1; -;
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 DR InterPro; IPR005094; Relaxase.
 DR Pfam; PF03432; Relaxase; 1.
 KW Plasmid.
 SQ SEQUENCE 899 AA; 103977 MW; E7DB0164C54914E3 CRC64;

QY 84 LKSANTGNNERIINVSIIKLRKPPSTNAGRRQKRL---TCP-----SCDSYKPKPK 134
 DB 92 SLETAADMEYI-----ARQAHYAKDDTDPVHYILSWQSHSPRPE 133
 QY 135 EFLERFKSLLOKM---IHQHLSSRTHGSEDS 162
 DB 134 QIYDSVRHTLKSGLADHQYVSA-VHTDTDN 163

RESULT 9
 Q9R2J7 PRELIMINARY; PRT; 899 AA.
 AC Q9R2J7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Relaxase.
 GN NIKB.
 OS Shigella sonnei.
 OG Plasmid Col1b-P9.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Shigella.
 OX NCBI_TaxID=624;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=P9;
 RA Sampei G., Mizobuchi K.;
 RT "Organization and diversification of plasmid genomes: complete
 nucleotide sequence of the Col1b-P9 genome";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB021078; BAA75140.1; -;
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 DR InterPro; IPR005094; Relaxase.
 DR Pfam; PF03432; Relaxase; 1.
 KW Plasmid.
 SQ SEQUENCE 899 AA; 103977 MW; E7DB0164C54914E3 CRC64;

Query Match 9.8%; Score 83; DB 2; Length 899;
 Best Local Similarity 22.5%; Pred. No. 10;
 Matches 34; Conservative 22; Mismatches 55; Indels 40; Gaps 7;

QY 27 SSSQCDRHMTMROLIIVOLKNYNDLVPPELPAPEDVETNCWSAF---SCFQKAQ 83
 DB 38 SSSQAEQPHRSRSLVDYATRLRN-----ESFVALVDVMKDCGEWVNFVGTVCFNCT 91
 QY 84 LKSANTGNNERIINVSIIKLRKPPSTNAGRRQKRL---TCP-----SCDSYKPKPK 134
 DB 92 SLETAADMEYI-----ARQAHYAKDDTDPVHYILSWQSHSPRPE 133
 QY 135 EFLERFKSLLOKM---IHQHLSSRTHGSEDS 162
 DB 134 QIYDSVRHTLKSGLADHQYVSA-VHTDTDN 163

RESULT 10
 Q8CPT9 PRELIMINARY; PRT; 1224 AA.
 AC Q8CPT9;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE ATP-dependent nuclease subunit A.
 GN SE0664.
 OS Staphylococcus epidermidis.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 12228;
 RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
 Chen Z., Wen Y.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE016746; AAO04261.1; -;

DR GO: GO:0005524; F-ATP binding; IEA.
 DR GO: GO:0004003; F-ATP dependent DNA helicase activity; IEA.
 DR GO: GO:0003677; F-DNA binding; IEA.
 DR GO: GO:0006281; P-DNA repair; IEA.
 DR InterPro: IPR000212; UvrD-helicase.
 DR Pfam: PF00580; UvrD-helicase; 1.
 KW Complete proteome.
 SQ SEQUENCE 1224 AA; 143015 MW; 4B204F41A1ADP6A1 CRC64;

Query Match 9.8%; Score 83; DB 16; Length 1224;
 Best Local Similarity 26.3%; Pred. No. 14;
 Matches 45; Conservative 22; Mismatches 60; Indels 44; Gaps 8;

QY 17 VIFLGTLV-HKSSQGDHMRVRLQIDVQLKYNVDLPFLPAPEDVETNCWSA 75
 Db 909 VLYGVLAHQSPSPNDQRFER-----DIDQLNSEVPRVIVIDYEDVSTEEVND 962
 QY 76 FSCFQKQAQKSAANTGNNRIINY-----SIKKLR-----KPPSTN 111
 Db 963 NEIRTEELKAINTEGVEDVKIKHQLSYDYPFKVNTMKPSQSVSELRQLETEESNTN 1022
 QY 112 AGPRQKRLTCSQCDSEYKPKPELRFK-----SILQKMIHQHLSR 155
 Db 1023 YDRVQYRI---GVASYSR--PK-FLTQPKKKAINEIGTMTVMQHLDFR 1067

RESULT 11
 Q9VYB8 PRELIMINARY; PRT; 566 AA.
 ID Q9VYB8 PRELIMINARY; PRT; 566 AA.
 AC Q9VYB8 PRELIMINARY; PRT; 566 AA.
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE CG15745 protein.
 GN CG15745
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely.
 RX MEDLINE=2019606; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt J.G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houshon K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mccarthy K.C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Sanders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M.C., Skupski M.P., Smith T.,

PA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 PA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 PA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J., Q.A.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Rao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhao G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003492; AAP48250.1;
 DR Flybase; FBgn0030469; CG15745.
 SQ SEQUENCE 566 AA; 60620 MW; 31FA41FA4AEF427F CRC64;

Query Match 9.6%; Score 81.5; DB 5; Length 566;
 Best Local Similarity 26.1%; Pred. No. 8.3;
 Matches 24; Conservative 21; Mismatches 40; Indels 7; Gaps 3;

QY 66 DVETNCWSAFS--CFQKQAQKSAANTGNNRIINYIKLKKPSTNAGRQKRLTCCP 123
 Db 120 DIGYPCVASISLALRKAQLKAQPFQNGV---GLARDSETSTTRITRTNRSAYP 175
 QY 124 SCDSEYKPKPELRFKPKSLL-QKMIHQHLS 154
 Db 176 SCTERGKPVQQLIDQFQAMIVQOQQOQLSN 207

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 AC Q8JFF4 PRELIMINARY; PRT; 140 AA.
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Interleukin-2 precursor (interleukin-15) (IL-15).
 GN IL-2.
 OS Anas platyrhynchos (Domestic duck).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
 OX NCBI_TaxID=8839;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Schmol K., Schultz U.;
 RT "Cloning and characterization of duck interleukin-2";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 EN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Splice;
 RA Zhou J.Y., Wang J.Y., Chen J.G., Cheng L.Q., Zheng X.J., Gong H.,
 RA Chen Q.X.;
 RT "Cloning and characterization of Shaoxing layer duck (China)
 RT interleukin-2";
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Sreekumar E., Premraj A., Rasool T.J.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
 CC LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15
 CC WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R
 CC GAMMA BUT NOT IL-2R ALPHA (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE IL-15 FAMILY.
 DR EMBL; AF294322; AA073551.1;
 DR EMBL; AF294323; AA073552.1;
 DR EMBL; AY173028; AA020087.1;
 DR EMBL; AY232490; AA046162.1;
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0005126; F:hematopoietin/interferon-class (D200-domain. .; IEA.
 DR GO: GO:0006955; P:immune response; IEA.
 DR InterPro: IPR003443; Interleukin_15.
 DR Pfam: PF02372; IL15; 1.
 KW Cytokine; Signal.
 FT SIGNAL 1
 CHAIN 22 140
 FT INTERLEUKIN-2.

RESULT 14

Q9VJL7 PRELIMINARY; PRT; 385 AA.

Q9VJL7
AC Q9VJL7
AC Q9VJL7
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
BG:DS02740.8 protein.
DE BG:DS02740.8 OR CGI7328.
GN Drosophila melanogaster (fruit fly).
OS Drosophila melanogaster
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Phylotroidea; Drosophilidae; Drosophila.
NCBI_TaxId=7227;
OX [1]
RN
RP
SEQUENCE FROM N.A.
STRAIN=Berkely;
MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.C., Wortman J.R., Fendell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J.P., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.N., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz N.S., Gelbart W.M., Glaesser K.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaesser K.,
RA Glödek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaisli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattai B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Smith H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svavskas R., Tector C., Turner K., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodgate T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zavari J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.-H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RT Science 287:2185-2195(2000).
DR EMBL; AR003650; AAF5316.1; --
DR HSP; F08046; IALI.
DR FlyBase; FBGN0028895; BG:DS02740.8

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DR PFAM: PF00096; 2f-C2H2; 5
DR SMART: SM00355; ZnF_C2H2; 6
DR PROSITE: PS00029; ZINC_FINGER_C2H2_1; 6
DR PROSITE: PS00151; ZINC_FINGER_C2H2_2; 6
DR KW Metal-binding; zinc; zinc-finger;
SQ SEQUENCE 385 AA; 43943 MW; 24D0EAE4C5FD5DA6 CRC64;
Query Match 9.5%; Score 81; DB 5; Length 385;
Best Local Similarity 22.3%; Ref. NO. 6;
Matches 37; Conservative 22; Mismatches 44; Indels 64; Gaps 9;
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Db 129 RKPPEEHKKRGPVPMPTCYECHKSFKCIQAULTQHI--RTHTGE 173

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Job time : 28.4706 secs

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67 NTD-----FVEKPLLPQSDSEEEFVDAKVK-----RRSR-----YQ 99
130 KPPKPEFLERFKSLLOKMIH-----OHLSSRTHGSE 160
100 RKPPEEHKKRGPVPMPTCYECHKSFKCIQAULTQHI--RTHTGE 144

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DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE BG:DS02740.8 protein.
GN BG:DS02740.8 OR CG17328.
OS Drosophila melanogaster. (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
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RC STRAIN=Berkely;
RX MEDLINE=99403001; PubMed=10471707;
RA Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
RA Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
RA Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
RA Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
RA Calniker S., Rubin G.M.,
RA "An exploration of the sequence of a 2.9-Mb region of the genome of
RT Drosophila melanogaster: the Adh region."
RL Genetics 153:179-219(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RA Calniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
RA Butenoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
RA Farfan D.E., Galle R., George R., Harris N.L., Hoskins R.A.,
RA Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
RA Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
RA Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
RA Sethi H., Snair E., Svirskaas R.R., Wan K.H., Weinburg T., Zhang R.,
RA Zieran L.L., Rubin G.M.,
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
EMBL; AE003415; AAF4998.1; -
DR HSP; P08046; IALI.
DR FlyBase; FBgn002895; BG:DS02740.8.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR007087; ZnF_C2H2.
DR Pfam; PF00096; zf-C2H2; 6.
DR SMART; SM00355; Znf_C2H2; 6.
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DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 6.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 414 AA; 47307 MW; 182657C92E2E2D1F CRC64;

Query Match 9.5%; Score 81; DB 5; Length 414;
Best Local Similarity 22.2%; Pred.No. 6.5;
Matches 37; Conservative 22; Mismatches 44; Indels 64; Gaps 9;
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QY 70 NCWSAFSCFQKQALKSANTGNNERIINVS1KKLRKPPSTNAGRRQKHRLTCFSCDSYE 129

GenCore version 5.1.6
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DM protein - protein search, using sw model

Run on: March 3, 2004, 12:33:10 ; Search time 11.3824 seconds
(without alignments)
734.770 Million cell updates/sec

Title: US-09-825-561a-10

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	850	100.0	162	4	US-09-923-246-2
3	850	100.0	162	4	US-10-295-723-2
4	695.5	81.8	519	4	US-09-522-217-85
5	695.5	81.8	519	4	US-09-923-246-85
6	695.5	81.8	519	4	US-10-295-723-85
7	486	57.2	146	4	US-09-522-217-56
8	486	57.2	146	4	US-09-923-246-56
9	486	57.2	146	4	US-10-295-723-56
10	394	46.4	510	4	US-09-522-217-89
11	394	46.4	510	4	US-09-923-246-89
12	394	46.4	510	4	US-10-295-723-89
13	212	24.9	40	4	US-09-522-217-72
14	212	24.9	40	4	US-09-923-246-72
15	212	24.9	40	4	US-10-295-723-72
16	176	20.7	32	4	US-09-522-217-73
17	176	20.7	32	4	US-09-923-246-73
18	176	20.7	32	4	US-10-295-723-73
19	99.5	11.7	114	1	US-08-031-399-6
20	99.5	11.7	114	1	US-08-031-399-12
21	99.5	11.7	114	1	US-08-393-305-3
22	99.5	11.7	114	1	US-08-726-817-3
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24	99.5	11.7	114	1	US-08-504-042-12
25	99.5	11.7	114	2	US-08-725-969-3
26	99.5	11.7	114	2	US-08-794-524-3
27	99.5	11.7	114	3	US-09-189-193-3

28	99.5	11.7	114	4	US-09-462-941-20	Sequence 20, Appli
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40	99.5	11.7	162	4	US-09-522-217-113	Sequence 113, App
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43	99.5	11.7	162	4	US-10-295-723-113	Sequence 113, App
44	99.5	11.7	162	5	PCT-US94-03793-5	Sequence 5, Appli
45	99.5	11.7	162	5	PCT-US96-06423-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-522-217-2
; Sequence 2, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: No. 6307024ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; EARLIER FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-522-217-2

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Gaps	0;						
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QY	121	TCPCDSDSYKKPKPKFLERPKSLLOKMIHQHLSRTHGSEDS	162				
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; Sequence 2, Application US/09923246
; Patent No. 6605272
; GENERAL INFORMATION:
; APPLICANT: No. 6605272ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-246-2

Query Match 100.0%; Score 850; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 1e-86;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGNMERIVICLVIFLGLTVHKSSSQGQDRMIRMRQLIDIVDQLKNYVNDLVPEF 60
Db 1 MRSSPGNMERIVICLVIFLGLTVHKSSSQGQDRMIRMRQLIDIVDQLKNYVNDLVPEF 60
QY 61 LPAPEDVETNCWSAFSCFQKALXSANTGNNERIINVSIKLKKPKPSTNAGRQKHL 120
Db 61 LPAPEDVETNCWSAFSCFQKALXSANTGNNERIINVSIKLKKPKPSTNAGRQKHL 120
QY 121 TCPSCDSYEKKPKPFLEFRFKSLLOQMTHQHLSSRTHGSEDS 162
Db 121 TCPSCDSYEKKPKPFLEFRFKSLLOQMTHQHLSSRTHGSEDS 162

RESULT 4
US-09-522-217-85
; Sequence 85, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: No. 6307024ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; CURRENT FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MBP-human zalphall ligand fusion polypeptide
US-09-522-217-85

Query Match 81.8%; Score 695.5; DB 4; Length 519;
Best Local Similarity 95.7%; Pred. No. 6.7e-69;
Matches 134; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 23 LVHKSSSQGQDRMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNCWSAFSCFQKA 82
Db 383 LVPRGS---QDRMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNCWSAFSCFQKA 439
QY 83 QLKXSANTGNNERIINVSIKLKKPKPSTNAGRQKHLTCPCSDSYEKKPKPFLEFRFKS 142

RESULT 3
US-10-295-723-2
; Sequence 2, Application US/10295723
; Patent No. 6686178
; GENERAL INFORMATION:
; APPLICANT: No. 6686178ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
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DB 440 QLKSA NTGN NRI I NVSIKKLRKP PSTNAGRRQKRLT C PSCDSYKCKPKF LERFKS 499

QY 143 L LQKMIHQHLSRTHGSEDS 162

DB 500 L LQKMIHQHLSRTHGSEDS 519

RESULT 5

US-09-923-246-85

; Sequence 85, Application US/09923246

; Patent No. 6605272

; GENERAL INFORMATION:

; APPLICANT: No. 6605272ak, Julia E.

; APPLICANT: Presnell, Scott R.

; APPLICANT: Sprecher, Cindy A.

; APPLICANT: Foster, Donald C.

; APPLICANT: Holly, Richard D.

; APPLICANT: Gross, Jane A.

; APPLICANT: Johnston, Janet V.

; APPLICANT: Nelson, Andrew J.

; APPLICANT: Dillon, Stacey R.

; APPLICANT: Hammond, Angela K.

; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND

; FILE REFERENCE: 99-16

; CURRENT APPLICATION NUMBER: US/09/923,246

; CURRENT FILING DATE: 2001-08-03

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217

; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01

; NUMBER OF SEQ ID NOS: 115

; SOFTWARE: PastSeq for Windows Version 3.0

; SEQ ID NO 85

; LENGTH: 519

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: MBP-human zalphall Ligand fusion polypeptide

US-09-923-246-85

Query Match 81.8%; Score 695.5; DB 4; Length 519;

Best Local Similarity 95.7%; Pred. No. 6.7e-69;

Matches 134; Conservative 1; Mismatches 2; Indels 3; Gaps 1

QY 23 LVHKSSQSDRHLMRQLDIVDLQKNYNDLVPELPAPEDVETNCWSAFSCFQKA 82

DB 383 LVFRGS---QDRHLMRQLDIVDLQKNYNDLVPELPAPEDVETNCWSAFSCFQKA 439

QY 83 QLKSA NTGN NRI I NVSIKKLRKP PSTNAGRRQKRLT C PSCDSYKCKPKF LERFKS 142

DB 440 QLKSA NTGN NRI I NVSIKKLRKP PSTNAGRRQKRLT C PSCDSYKCKPKF LERFKS 499

QY 143 L LQKMIHQHLSRTHGSEDS 162

DB 500 L LQKMIHQHLSRTHGSEDS 519

RESULT 6

US-10-295-723-85

; Sequence 85, Application US/10295723

; Patent No. 6686178

; GENERAL INFORMATION:

; APPLICANT: No. 6686178ak, Julia E.

; APPLICANT: Presnell, Scott R.

; APPLICANT: Sprecher, Cindy A.

; APPLICANT: Foster, Donald C.

; APPLICANT: Holly, Richard D.

; APPLICANT: Gross, Jane A.

; APPLICANT: Johnston, Janet V.

; APPLICANT: Nelson, Andrew J.

```
Query Match      57.2%; Score 486; DB 4; Length 146;
Best Local Similarity 63.0%; Pred. No. 2.5e-46;
Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

QY 8 MERIVICLVIFLGTLVHKSOGQDRHMIRMQLDIVDQKNVYNDLVPEFLPAPEDV 67
DB 1 MERTVCLVIFLGTVAHKSPOGPDRLRLRHLDIVDQKIYENDLDPILLSAPQDV 60
QY 68 ETNCWEAFSCFQKQAKLSANTGNRIINVS:KKLKRKPPSTNAGRQKRLTSPSCDS 127
DB 61 KGHCEHAFAFCQKAKLPSPGNKTFIIDLVAQLRRRLPARRGGKKQKHIAKPCSDS 120
QY 128 YEKKPPKEFLERFKSLQKMIHQHLS 153
DB 121 YEKRTPKFLERLKWLQKMIHQHLS 146

RESULT 8
US-09-923-246-56
; Sequence 56, Application US/09923246
; Patent No. 6605272
; GENERAL INFORMATION:
; APPLICANT: No. 6605272ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillion, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 146
; TYPE: PRT
; ORGANISM: mus musculus
US-09-923-246-56

Query Match      57.2%; Score 486; DB 4; Length 146;
Best Local Similarity 63.0%; Pred. No. 2.5e-46;
Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

QY 8 MERIVICLVIFLGTLVHKSOGQDRHMIRMQLDIVDQKNVYNDLVPEFLPAPEDV 67
DB 1 MERTVCLVIFLGTVAHKSPOGPDRLRLRHLDIVDQKIYENDLDPILLSAPQDV 60
QY 68 ETNCWEAFSCFQKQAKLSANTGNRIINVS:KKLKRKPPSTNAGRQKRLTSPSCDS 127
DB 61 KGHCEHAFAFCQKAKLPSPGNKTFIIDLVAQLRRRLPARRGGKKQKHIAKPCSDS 120
QY 128 YEKKPPKEFLERFKSLQKMIHQHLS 153
DB 121 YEKRTPKFLERLKWLQKMIHQHLS 146

RESULT 9
US-10-295-723-56
; Sequence 56, Application US/10295723
; Patent No. 6686178
; GENERAL INFORMATION:
```

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; APPLICANT: No. 6686178ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillion, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 146
; TYPE: PRT
; ORGANISM: mus musculus
US-10-295-723-56

Query Match      57.2%; Score 486; DB 4; Length 146;
Best Local Similarity 63.0%; Pred. No. 2.5e-46;
Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

QY 8 MERIVICLVIFLGTLVHKSOGQDRHMIRMQLDIVDQKNVYNDLVPEFLPAPEDV 67
DB 1 MERTVCLVIFLGTVAHKSPOGPDRLRLRHLDIVDQKIYENDLDPILLSAPQDV 60
QY 68 ETNCWEAFSCFQKQAKLSANTGNRIINVS:KKLKRKPPSTNAGRQKRLTSPSCDS 127
DB 61 KGHCEHAFAFCQKAKLPSPGNKTFIIDLVAQLRRRLPARRGGKKQKHIAKPCSDS 120
QY 128 YEKKPPKEFLERFKSLQKMIHQHLS 153
DB 121 YEKRTPKFLERLKWLQKMIHQHLS 146

RESULT 10
US-09-522-217-89
; Sequence 89, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: No. 6307024ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillion, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; CURRENT FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
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SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 89

LENGTH: 510

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: MBP-mouse zalphall1 Ligand fusion polypeptide

US-09-522-217-89

Query Match 46.4%; Score 394; DB 4; Length 510;

Best Local Similarity 62.0%; Pred. No. 2e-35;

Matches 75; Conservative 19; Mismatches 27; Indels 0; Gaps 0;

33 DRHMIRQLDIDVDQKNYVNDLPPELPAPEDVETNCWSAFSCFQKALKSANTGNN 92

390 DRLIRLRHLIDIVQLKIYENDLPDLSAPQDVKGCHHAFAAFACFQKALKPSNPGNN 449

93 ERIINVSIKKLKRPSTNAGRRQKRLTCDSCDSYKKPKPEFLERFKSLLOKMIHOHL 152

450 KTFIDLVLAQLRRRLPARRGGKKQKHIACPCSDSYEKRTPKPEFLERLKLQKMIHOHL 509

153 S 153

510 S 510

RESULT 11

US-09-923-246-89

Sequence 89, Application US/09923246

Patent No. 6605272

GENERAL INFORMATION:

APPLICANT: No. 6605272ak, Julia E.

APPLICANT: Presnell, Scott R.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Foster, Donald C.

APPLICANT: Holly, Richard D.

APPLICANT: Gross, Jane A.

APPLICANT: Johnston, Janet V.

APPLICANT: Nelson, Andrew J.

APPLICANT: Dillon, Stacey R.

APPLICANT: Hammond, Angela K.

TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL1 LIGAND

FILE REFERENCE: 99-16

CURRENT APPLICATION NUMBER: US/09/923,246

PRIOR FILING DATE: 2001-08-03

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217

PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904

PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013

PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01

NUMBER OF SEQ ID NOS: 115

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 89

LENGTH: 510

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: MBP-mouse zalphall1 Ligand fusion polypeptide

US-09-923-246-89

Query Match 46.4%; Score 394; DB 4; Length 510;

Best Local Similarity 62.0%; Pred. No. 2e-35;

Matches 75; Conservative 19; Mismatches 27; Indels 0; Gaps 0;

33 DRHMIRQLDIDVDQKNYVNDLPPELPAPEDVETNCWSAFSCFQKALKSANTGNN 92

390 DRLIRLRHLIDIVQLKIYENDLPDLSAPQDVKGCHHAFAAFACFQKALKPSNPGNN 449

93 ERIINVSIKKLKRPSTNAGRRQKRLTCDSCDSYKKPKPEFLERFKSLLOKMIHOHL 152

450 KTFIDLVLAQLRRRLPARRGGKKQKHIACPCSDSYEKRTPKPEFLERLKLQKMIHOHL 509

153 S 153

510 S 510

RESULT 13

US-09-522-217-72

Sequence 72, Application US/09522217

Patent No. 6307024

GENERAL INFORMATION:

APPLICANT: No. 6307024ak, Julia E.

APPLICANT: Presnell, Scott R.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Foster, Donald C.

APPLICANT: Gross, Jane A.

APPLICANT: Johnston, Janet V.

APPLICANT: Nelson, Andrew J.

APPLICANT: Dillon, Stacey R.

QY 153 S 153

DB 510 S 510

RESULT 12

US-10-295-723-89

Sequence 89, Application US/10295723

Patent No. 6686178

GENERAL INFORMATION:

APPLICANT: No. 6686178ak, Julia E.

APPLICANT: Presnell, Scott R.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Foster, Donald C.

APPLICANT: Holly, Richard D.

APPLICANT: Gross, Jane A.

APPLICANT: Johnston, Janet V.

APPLICANT: Nelson, Andrew J.

APPLICANT: Dillon, Stacey R.

APPLICANT: Hammond, Angela K.

TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL1 LIGAND

FILE REFERENCE: 99-16

CURRENT APPLICATION NUMBER: US/10/295,723

PRIOR FILING DATE: 2002-11-15

PRIOR APPLICATION NUMBER: 09/522,217

PRIOR FILING DATE: 2000-03-09

PRIOR APPLICATION NUMBER: US 60/123,547

PRIOR FILING DATE: 1999-03-09

PRIOR APPLICATION NUMBER: US 60/123,904

PRIOR FILING DATE: 1999-03-11

PRIOR APPLICATION NUMBER: US 60/142,013

PRIOR FILING DATE: 1999-07-01

NUMBER OF SEQ ID NOS: 115

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 89

LENGTH: 510

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: MBP-mouse zalphall1 Ligand fusion polypeptide

US-10-295-723-89

Query Match 46.4%; Score 394; DB 4; Length 510;

Best Local Similarity 62.0%; Pred. No. 2e-35;

Matches 75; Conservative 19; Mismatches 27; Indels 0; Gaps 0;

33 DRHMIRQLDIDVDQKNYVNDLPPELPAPEDVETNCWSAFSCFQKALKSANTGNN 92

390 DRLIRLRHLIDIVQLKIYENDLPDLSAPQDVKGCHHAFAAFACFQKALKPSNPGNN 449

93 ERIINVSIKKLKRPSTNAGRRQKRLTCDSCDSYKKPKPEFLERFKSLLOKMIHOHL 152

450 KTFIDLVLAQLRRRLPARRGGKKQKHIACPCSDSYEKRTPKPEFLERLKLQKMIHOHL 509

153 S 153

510 S 510

APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/522,217
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/142,013
EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 72
LENGTH: 40
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Huzalpalh1L-1 peptide
US-09-522-217-72

Query Match 24.9%; Score 212; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 QDRHMIRQLIDIVDQKNVNDLVPEFLPAPEDVETNC 71
DB 1 QDRHMIRQLIDIVDQKNVNDLVPEFLPAPEDVETNC 40

RESULT 14
US-09-923-246-72
Sequence 72, Application US/09923246
Patent No. 6605272
GENERAL INFORMATION:
APPLICANT: No. 6605272ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/923,246
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 72
LENGTH: 40
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Huzalpalh1L-1 peptide
US-09-923-246-72

Query Match 24.9%; Score 212; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 QDRHMIRQLIDIVDQKNVNDLVPEFLPAPEDVETNC 71
DB 1 QDRHMIRQLIDIVDQKNVNDLVPEFLPAPEDVETNC 40

RESULT 15
US-10-295-723-72
Sequence 72, Application US/10295723
Patent No. 6686178
GENERAL INFORMATION:
APPLICANT: No. 6686178ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/10/295,723
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 09/522,217
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 72
LENGTH: 40
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Huzalpalh1L-1 peptide
US-10-295-723-72

Query Match 24.9%; Score 212; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 QDRHMIRQLIDIVDQKNVNDLVPEFLPAPEDVETNC 71
DB 1 QDRHMIRQLIDIVDQKNVNDLVPEFLPAPEDVETNC 40

Search completed: March 3, 2004, 12:39:56
Job time : 12.3824 secs

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OM protein - protein search, using sw model

Run on: March 3, 2004, 12:38:15 ; Search time 21.1765 Seconds
(without alignments)
1615.322 Million cell updates/sec

Title: US-09-825-561A-10

Perfect score: 850

Sequence: 1 MRSSPGNMRIVICLWIFL.....LLQXIHHLSTRTHGSEDS 162

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgm2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgm2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgm2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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- 5: /cgm2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgm2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgm2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgm2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgm2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgm2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgm2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgm2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgm2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgm2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgm2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgm2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	850	100.0	162	9	US-09-923-246-2
2	850	100.0	162	9	US-09-825-561A-10
3	850	100.0	162	10	US-09-972-218A-19
4	850	100.0	162	14	US-10-264-634-19
5	850	100.0	162	14	US-10-295-723-2
6	850	100.0	162	14	US-10-282-622-2
7	850	100.0	162	15	US-10-456-780-2
8	831	97.8	162	14	US-10-282-622-6
9	758	89.2	147	14	US-10-282-622-4
10	695.5	81.8	519	9	US-09-923-246-85
11	695.5	81.8	519	14	US-10-295-723-85
12	486	57.2	146	9	US-09-923-246-56
13	486	57.2	146	9	US-09-825-561A-47
14	486	57.2	146	14	US-10-295-723-56
15	486	57.2	146	15	US-10-456-780-4

16	394	46.4	510	9	US-09-923-246-89	Sequence 89, Appl
17	394	46.4	510	14	US-10-295-723-89	Sequence 89, Appl
18	212	24.9	40	9	US-09-923-246-72	Sequence 72, Appl
19	212	24.9	40	14	US-10-235-723-72	Sequence 72, Appl
20	176	20.7	32	9	US-09-923-246-73	Sequence 73, Appl
21	176	20.7	32	14	US-10-295-723-73	Sequence 73, Appl
22	99.5	11.7	114	14	US-10-400-377-20	Sequence 20, Appl
23	99.5	11.7	114	14	US-10-400-708-20	Sequence 20, Appl
24	99.5	11.7	114	14	US-10-298-148-20	Sequence 20, Appl
25	99.5	11.7	162	9	US-09-953-323A-4	Sequence 4, Appl
26	99.5	11.7	162	9	US-09-855-313A-4	Sequence 4, Appl
27	99.5	11.7	162	9	US-09-923-246-113	Sequence 113, Appl
28	99.5	11.7	162	14	US-10-245-243-6	Sequence 113, Appl
29	99.5	11.7	162	14	US-10-295-723-113	Sequence 9, Appl
30	99.5	11.7	162	14	US-10-282-622-9	Sequence 9, Appl
31	99.5	11.7	162	15	US-10-456-780-9	Sequence 2, Appl
32	99.5	11.7	162	16	US-10-275-620-2	Sequence 3, Appl
33	94.5	11.1	122	14	US-10-385-072-3	Sequence 2, Appl
34	94.5	11.1	162	9	US-09-953-323A-2	Sequence 2, Appl
35	94.5	11.1	162	9	US-09-855-313A-2	Sequence 8, Appl
36	94.5	11.1	162	14	US-10-245-243-8	Sequence 6, Appl
37	91.5	10.8	337	9	US-09-899-980A-6	Sequence 48, Appl
38	91.5	10.8	337	14	US-10-004-633-48	Sequence 49, Appl
39	91.5	10.8	342	14	US-10-004-633-41	Sequence 41, Appl
40	91.5	10.8	567	9	US-09-899-980A-7	Sequence 7, Appl
41	91.5	10.8	567	14	US-10-011-548-34	Sequence 39, Appl
42	91.5	10.8	567	14	US-10-004-633-39	Sequence 639, Appl
43	91.5	10.8	567	14	US-10-101-464A-639	Sequence 939, Appl
44	77	9.1	139	14	US-10-101-464A-939	
45	76	8.9	400	14	US-10-101-464A-939	

ALIGNMENTS

RESULT 1

US-09-923-246-2
; Sequence 2: Application US/09923246
; Patent No. US20020128446A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020128446Alak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-246-2

Query Match 100.0%; Score 850; DB 9; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.8e-84;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MRSSPGNMRIVICLWIFLVLGTLVHKSSQGDHMRMRQLDIVDQLKNYVNDIVPEF 60

1	MRSPGNRIRIVICLWVIFGLTVHKSSSQQRHMRQLDIDVDQKYNVDLVPF	60
61	LPAPEDVETNCWGAFCFQKAQKKSANTGNRIINVSIGKLRKPPSTNAGRQKRL	120
61	LPAPEDVETNCWGAFCFQKAQKKSANTGNRIINVSIGKLRKPPSTNAGRQKRL	120
121	TCPCSDSYEKPKPKFEFLERFKSLQKMIHQHLSRTHGSEDS	162
121	TCPCSDSYEKPKPKFEFLERFKSLQKMIHQHLSRTHGSEDS	162

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RESULT 2
US-09-825-561A-10
; Sequence 10, Application US/09825561A
; Patent No. US2002013767A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No US2002013767A1ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHALL1 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 162
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-825-561A-10

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	Query Match	100.0%	Score 850;	DB 9;	Length 162;
	Best Local Similarity	100.0%	Pred. No. 1.8e-84;		
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DB	1	MRSSPGNNRIVICLMVIFIGTLVHKSSSQGQRHMRQLDIDVDLQKNVNDLVEEP	60		
QY	61	LPAPEDVETNCWGAFCFQAKQLKSANTGNRIINVSICKLKRKPSTNAGRQKRL	120		
DB	61	LPAPEDVETNCWGAFCFQAKQLKSANTGNRIINVSICKLKRKPSTNAGRQKRL	120		
QY	121	TCPSCDSEYKKPPKEFTLPERFKSLQKMIHQHLSRSRTHGSEDS	162		
DB	121	TCPSCDSEYKKPPKEFTLPERFKSLQKMIHQHLSRSRTHGSEDS	162		

RESULT 3
US-09-972-218A-19
; Sequence 19, Application US/09972218A
; Publication No. US20030049798A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Laura
; APPLICANT: Whitters, Matthew J
; APPLICANT: Collins, Mary
; APPLICANT: Young, Deborah A.
; APPLICANT: Donaldson, Debra D.
; APPLICANT: Lowe, Leslie D.
; APPLICANT: Unger, Michelle
; TITLE OF INVENTION: MU-1, Member of the Cytokine Receptor Family
; FILE REFERENCE: 22058-553CIP2
; CURRENT APPLICATION NUMBER: US/09/972, 218A
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 09/569384

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; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 09/560766
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US/6057128
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: 08/057128
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Human
US-09-972-218A-19

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	Query Match	100.0%;	Score 850;	DB 10;	Length 162;
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Db	1	MRSPGNGMERIVICLMVIFLGTULVHKSSQGDHRMIRQLIDIVDLKKNVNDLVEF	60		
QY	61	LPAPEDVETNCWSAFSCFQAKLSANTGNNRIINVSISKLRKPPSTNAGRQKHRL	120		
Db	61	LPAPEDVETNCWSAFSCFQAKLSANTGNNRIINVSISKLRKPPSTNAGRQKHRL	120		
QY	121	TCPCSDSYKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS	162		
Db	121	TCPCSDSYKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS	162		

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RESULT 4,
US-10-264-634-19
,, Sequence 19, Application US/10264634
,, Publication No. US20030108549A1
,, GENERAL INFORMATION:
,, APPLICANT: Donaldson, Debra et al.
,, TITLE OF INVENTION: Methods and Compositions
,, FILE REFERENCE: G15320-P3
,, CURRENT APPLICATION NUMBER: US/10/264,634
,, CURRENT FILING DATE: 2002-10-04
,, PRIOR APPLICATION NUMBER: 09/040,005
,, PRIOR FILING DATE: 1998-03-17
,, PRIOR APPLICATION NUMBER: 09/560,766
,, PRIOR FILING DATE: 2000-04-28
,, PRIOR APPLICATION NUMBER: 09/569,384
,, PRIOR FILING DATE: 2000-05-11
,, PRIOR APPLICATION NUMBER: 09/972,218
,, PRIOR FILING DATE: 2001-10-04
,, PRIOR APPLICATION NUMBER: 60/373,746
,, PRIOR FILING DATE: 2002-04-17
,, NUMBER OF SEQ ID NOS: 44
,, SOFTWARE: PatentIn version 3.1
,, SEQ ID NO 19
,, LENGTH: 162
,, TYPE: PRT
,, ORGANISM: Human
,, US-10-264-634-19

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Query Match	100.0%	Score 850;	DB 14;	Length 162;
Best Local Similarity	100.0%;	Pred. NO. 1.8e-84;		
Matches 162;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	1	MRSSGNNRIVICLWIFLIGTLVHKSSSQGDHRIMRQLLIDIVDQKNYYNDLVPEF 60		
Db	1	MRSSGNNRIVICLWIFLIGTLVHKSSSQGDHRIMRQLLIDIVDQKNYYNDLVPEF 60		
QY	61	LPAPDEVTCNEWAFSCFOKAQLKSANTGNNRIINVSICKLKRKPPSTNAGRQKHRL 120		
Db	61	LPAPDEVTCNEWAFSCFOKAQLKSANTGNNRIINVSICKLKRKPPSTNAGRQKHRL 120		
QY	121	TCPCSDSYEKPPKEFLERFKSLLOKMIHOHLSRTHGSEDS 162		
Db	121	TCPCSDSYEKPPKEFLERFKSLLOKMIHOHLSRTHGSEDS 162		

GENERAL INFORMATION:
; APPLICANT: No. US20020128446Alak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Neilson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MBP-human zalphall1 Ligand fusion polypeptide
US-09-923-246-85

Query Match 81.8%; Score 695.5; DB 9; Length 519;
Best Local Similarity 95.7%; Pred. No. 5.4e-67;
Matches 134; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

Qy 23 LVKSSQGGQDRHMRQLDIVDQKYNVNDLVPEFLPAPEDVETNCWSAFSCFQKA 82
Db 383 LVPRGS---QDRHMRQLDIVDQKYNVNDLVPEFLPAPEDVETNCWSAFSCFQKA 439
Qy 83 QLKXANTGNRRINVSIIKLGKPPSTNAGRQKRLTQPCSDSYEKPPKPEFLERPKS 142
Db 440 QLKXANTGNRRINVSIIKLGKPPSTNAGRQKRLTQPCSDSYEKPPKPEFLERPKS 499
Qy 143 LQKMIHQHLSRTHGSEDS 162
Db 500 LQKMIHQHLSRTHGSEDS 519

RESULT 11
US-10-295-723-85
; Sequence 85, Application US/10295723
; Publication No. US2003012554A1
; GENERAL INFORMATION:
; APPLICANT: No. US2003012554A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Neilson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11

Query Match 89.2%; Score 758; DB 14; Length 147;
Best Local Similarity 98.6%; Pred. No. 1.6e-74;
Matches 145; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MRSPGNMERIVICLWVIFGLTVHKSSQGGQDRHMRQLDIVDQKYNVNDLVPEF 60
Db 1 MDSPGNMERIVICLWVIFGLTVHKSSQGGQDRHMRQLDIVDQKYNVNDLVPEF 60
Qy 61 LPAPEDVETNCWSAFSCFQKALKSANTGNRRINVSIIKLGKPPSTNAGRQKRL 120
Db 61 LPAPEDVETNCWSAFSCFQKALKSANTGNRRINVSIIKLGKPPSTNAGRQKRL 120
Qy 121 TCPSCDSYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
Db 121 TCPSCDSYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 9
US-10-282-622-4
; Sequence 4, Application US/10282622
; Publication No. US20030134390A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: West, James W.
; APPLICANT: No. US20030134390Alak, Julia E.
; TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/10/282,622
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: zalphall1 ligand Q153DT/I156D
US-10-282-622-4

Query Match 89.2%; Score 758; DB 14; Length 147;
Best Local Similarity 98.6%; Pred. No. 1.6e-74;
Matches 145; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MRSPGNMERIVICLWVIFGLTVHKSSQGGQDRHMRQLDIVDQKYNVNDLVPEF 60
Db 1 MDSPGNMERIVICLWVIFGLTVHKSSQGGQDRHMRQLDIVDQKYNVNDLVPEF 60
Qy 61 LPAPEDVETNCWSAFSCFQKALKSANTGNRRINVSIIKLGKPPSTNAGRQKRL 120
Db 61 LPAPEDVETNCWSAFSCFQKALKSANTGNRRINVSIIKLGKPPSTNAGRQKRL 120
Qy 121 TCPSCDSYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 147
Db 121 TCPSCDSYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 147

RESULT 10
US-09-923-246-85
; Sequence 85, Application US/09923246
; Patent No. US20020128446A1

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; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MBP-human zalphall1 Ligand fusion polypeptide
US-10-295-723-85

Query Match      81.8%; Score 695.5; DB 14; Length 519;
Best Local Similarity 95.7%; Pred. No. 5.4e-67;
Matches 134; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 23 LVKSSSGQDHRMIRKQLIDIVDQKNYVNDLVPEFLPAPEDVETNCWSAFSCFQKA 82
Db 383 LVPGS---QDRHMRKQLIDIVDQKNYVNDLVPEFLPAPEDVETNCWSAFSCFQKA 439

QY 83 QLKSAANTGNRIINVSIKKLRKPPSTNAGRROKHLRTPSCDSYSEKKPKPEFLERPKS 142
Db 440 QLKSAANTGNRIINVSIKKLRKPPSTNAGRROKHLRTPSCDSYSEKKPKPEFLERPKS 499

QY 143 LLQKMIHQHLSRTHGSEDS 162
Db 500 LLQKMIHQHLSRTHGSEDS 519

RESULT 12
US-09-923-246-56
; Sequence 56, Application US/09923246
; Patent No. US20020128446A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL1 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 146
; TYPE: PRT
; ORGANISM: mus musculus
US-09-923-246-56

Query Match      57.2%; Score 486; DB 9; Length 146;
Best Local Similarity 63.0%; Pred. No. 6.6e-45;
Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

QY 8 MERIVICLVIFLGTLVKSSSQGDHRMIRKQLIDIVDQKNYVNDLVPEFLPAPEDV 67
Db 1 MERTLVCLVIFLGTVAHKSPPQGPDRLLIRLRLHLDIVDQKIYENDLDPILLSAPQDV 60

QY 68 ETNCEWSAFSCFQAKLKSANTGNRIINVSIKKLRKPPSTNAGRROKHLRTPSCDS 127
Db 61 KGHCEHAFAFCFQAKLKPSPGNKNTFIIDVAQLRRLPARRGGKKQKHIACPCSDS 120

RESULT 13
US-09-825-561A-47
; Sequence 47, Application US/09825561A
; Patent No. US20020137677A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. US20020137677A1ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHALL1 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 47
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-825-561A-47

Query Match      57.2%; Score 486; DB 9; Length 146;
Best Local Similarity 63.0%; Pred. No. 6.6e-45;
Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

QY 8 MERIVICLVIFLGTLVKSSSQGDHRMIRKQLIDIVDQKNYVNDLVPEFLPAPEDV 67
Db 1 MERTLVCLVIFLGTVAHKSPPQGPDRLLIRLRLHLDIVDQKIYENDLDPILLSAPQDV 60

QY 68 ETNCEWSAFSCFQAKLKSANTGNRIINVSIKKLRKPPSTNAGRROKHLRTPSCDS 127
Db 61 KGHCEHAFAFCFQAKLKPSPGNKNTFIIDVAQLRRLPARRGGKKQKHIACPCSDS 120

RESULT 14
US-10-295-723-56
; Sequence 56, Application US/10295723
; Publication No. US20030125524A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030125524A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL1 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
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QY 128 YEKPPKEFLERFKSLQKMIHQHLS 153
Db 121 YEKPTPKFELERLKWLLQKMIHQHLS 146

RESULT 13
US-09-825-561A-47
; Sequence 47, Application US/09825561A
; Patent No. US20020137677A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. US20020137677A1ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHALL1 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 47
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-825-561A-47

Query Match      57.2%; Score 486; DB 9; Length 146;
Best Local Similarity 63.0%; Pred. No. 6.6e-45;
Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

QY 8 MERIVICLVIFLGTLVKSSSQGDHRMIRKQLIDIVDQKNYVNDLVPEFLPAPEDV 67
Db 1 MERTLVCLVIFLGTVAHKSPPQGPDRLLIRLRLHLDIVDQKIYENDLDPILLSAPQDV 60

QY 68 ETNCEWSAFSCFQAKLKSANTGNRIINVSIKKLRKPPSTNAGRROKHLRTPSCDS 127
Db 61 KGHCEHAFAFCFQAKLKPSPGNKNTFIIDVAQLRRLPARRGGKKQKHIACPCSDS 120

RESULT 14
US-10-295-723-56
; Sequence 56, Application US/10295723
; Publication No. US20030125524A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030125524A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL1 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
```

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; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 146
; TYPE: PRT
; ORGANISM: mus musculus
US-10-295-723-56

Query Match      57.2%; Score 486; DB 14; Length 146;
Best Local Similarity 63.0%; Pred. No. 6.6e-45;
Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

QY 8 MERIVICLVIFLGTVAHKSQGDHMRQLIDIVDLKYYNDLVPEFLPAPEDV 67
DB 1 MERTLVCLVIFLGTVAHKSQGDHMRQLIDIVDLKYYNDLVPEFLPAPEDV 60

QY 68 ETNCEWAFSCFQKALKSANTGNRIINVSIKLKRKPPSTNAGRQKRLTCPSGDS 127
DB 61 KGHCEHAFAACFQKALKSANTGNRIINVSIKLKRKPPSTNAGRQKRLTCPSGDS 120

QY 128 YEKPPKEFLERFKSLQKMIHQHLS 153
DB 121 YEKRTPKFELRLKWLQKMIHQHLS 146

RESULT 15
US-10-456-780-4
; Sequence 4, Application US/10456780
; Publication No. US20040009150A1
; GENERAL INFORMATION:
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Hughes, Steven D.
; APPLICANT: Holly, Richard D.
; TITLE OF INVENTION: USE OF IL-21 IN CANCER AND
; TITLE OF INVENTION: OTHER THERAPEUTIC APPLICATIONS
; FILE REFERENCE: 03-08
; CURRENT APPLICATION NUMBER: US/10/456,780
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/387,127
; PRIOR FILING DATE: 2002-06-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-456-780-4

Query Match      57.2%; Score 486; DB 15; Length 146;
Best Local Similarity 63.0%; Pred. No. 6.6e-45;
Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

QY 8 MERIVICLVIFLGTVAHKSQGDHMRQLIDIVDLKYYNDLVPEFLPAPEDV 67
DB 1 MERTLVCLVIFLGTVAHKSQGDHMRQLIDIVDLKYYNDLVPEFLPAPEDV 60

QY 68 ETNCEWAFSCFQKALKSANTGNRIINVSIKLKRKPPSTNAGRQKRLTCPSGDS 127
DB 61 KGHCEHAFAACFQKALKSANTGNRIINVSIKLKRKPPSTNAGRQKRLTCPSGDS 120

QY 128 YEKPPKEFLERFKSLQKMIHQHLS 153
DB 121 YEKRTPKFELRLKWLQKMIHQHLS 146

Search completed: March 3, 2004, 12:50:52
Job time : 22.1765 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 3, 2004, 12:24:04 ; Search time 38.6471 Seconds
(without alignments)

1184.377 Million cell updates/sec

Title: US-09-825-561a-10

Perfect score: 850

Sequence: 1 MRSPGNRIVICLMVFL.....LQKMIHQLSRRHSGSDS 162

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_29Jan04:*
1: geneseq1980s:*
2: geneseq1990s:*
3: geneseq2000s:*
4: geneseq2001s:*
5: geneseq2002s:*
6: geneseq2003as:*
7: geneseq2003bs:*
8: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	DB ID	Description
1	850	100.0	162	3 AAB18623	Aab18623 A human z
2	850	100.0	162	5 AAE13729	Aae13729 Human sol
3	850	100.0	162	5 AAU11965	Aau11965 Human zal
4	850	100.0	162	6 ABR61407	Abr61407 Human IL-
5	850	100.0	162	7 AAE14932	Aae14932 Human int
6	850	100.0	162	7 ABU62893	Abu62893 Human int
7	850	100.0	162	7 ADE85808	Ade85808 Human int
8	831	97.8	162	7 AAE14934	Aae14934 Human int
9	758	89.2	147	7 AAE14933	Aae14933 Human int
10	695.5	81.8	519	3 AAB18627	Aab18627 Amino aci
11	695.5	81.8	519	5 AAU11971	Aau11971 MBP-human
12	486	57.2	146	3 AAB18624	Aab18624 A mouse z
13	486	57.2	146	5 AAE13737	Aae13737 Murine so
14	486	57.2	146	5 AAU11968	Aau11968 Mouse zal
15	486	57.2	146	7 ADE85809	Ade85809 Murine in
16	486	57.2	379	7 ADE85818	Ade85818 Murine in
17	481	56.6	146	7 ADE85806	Ade85806 Murine in
18	476	56.0	146	7 ADE85807	Ade85807 Murine mu
19	476	56.0	379	7 ADE85820	Ade85820 Murine mu
20	394	46.4	510	3 AAB18628	Aab18628 Amino aci
21	394	46.4	510	5 AAU11972	Aau11972 MBP-mouse
22	212	24.9	40	3 AAB18625	Aab18625 Antigenin
23	212	24.9	40	5 AAU11969	Aau11969 Human zal
24	176	20.7	32	3 AAB18626	Aab18626 Antigenin
25	176	20.7	32	5 AAU11970	Aau11970 Human zal

ALIGNMENTS

RESULT 1

AAB18623
ID AAB18623 standard; protein; 162 AA.

AC AAB18623;

DT 22-JAN-2001 (first entry)

DE A human zalphall ligand polypeptide.

XX zalphall ligand; cytokine; haematopoietic cell proliferation; lymphoma;
KW tumorigenesis; leukaemia; hematopoiesis; B cell tumour.

OS Homo sapiens.

PN W0200053761-A2.

PD 14-SEP-2000.

XX 09-MAR-2000; 2000WO-US006067.

PR 09-MAR-1999; 99US-00264908.

PR 11-MAR-1999; 99US-00265992.

PR 01-JUL-1999; 99US-0142013P.

XX (ZYMO) ZYMOGENETICS INC.

XX Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;

XX Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;

XX WPI: 2000-565600/52.

XX N-PSDB; AAB75552.

XX New human cytokine, designated zalphall ligand, useful for stimulating
PT the proliferation and/or development of hematopoietic cells in vitro and
PT in vivo, and for treating tumorigenesis.

XX Disclosure; Page 205-206; 256pp; English.

XX The present sequence represents a human zalphall ligand polypeptide,
CC which is a cytokine. The zalphall ligand is useful for stimulating the
CC proliferation and development of hematopoietic cells in vitro and in
CC vivo. Zalphall ligand polynucleotides can be used as primers or probes
CC for cloning the zalphall gene. The zalphall ligand is useful for treating
CC tumorigenesis. A zalphall ligand-saporin fusion toxin may be used for
CC treating leukaemias and lymphomas. Antagonists against zalphall ligand
CC are useful as research reagents for characterizing ligand-receptor
CC interaction. Antagonists are also useful for inhibiting expansion,

CC proliferation, activation and differentiation of cells involved in
 CC regulating hematopoiesis. The zalphall ligand may also be used to
 CC stimulate an immune response against B cell tumour, a virus, a parasite
 CC or a bacterium. The zalphall polypeptides, polynucleotides, antagonists,
 CC agonists and antibodies are also useful for the detection, diagnosis,
 CC prevention, and treatment of diseases associated with a zalphall ligand
 CC genetic defect
 XX Sequence 162 AA;
 SQ

Query Match 100.0%; Score 850; DB 3; Length 162;
 Best Local Similarity 100.0%; Pred. No. 1.3e-86;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGNMERIVICLMVIFLGLTVHKSSQGGDRHMRQLIDVDQLKNYNDLVPEF 60
 DB 1 MRSSPGNMERIVICLMVIFLGLTVHKSSQGGDRHMRQLIDVDQLKNYNDLVPEF 60

QY 61 LPAPEDVETNCEWSAFSCFQKQALKSANTGNNERIINVSIKKLKRKPPSTNAGRQKHL 120
 DB 61 LPAPEDVETNCEWSAFSCFQKQALKSANTGNNERIINVSIKKLKRKPPSTNAGRQKHL 120

QY 121 TCPSCDSYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
 DB 121 TCPSCDSYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 2
 AAEL13729
 ID AAE13729 standard; protein; 162 AA.
 XX
 AC AAEL13729;
 DT 26-FEB-2002 (first entry)
 XX
 DE Human soluble Zalphall cytokine receptor ligand protein.
 XX
 KW Human; Zalphall; cytokine receptor; immunosuppressive; cytostatic;
 KW inflammatory disorder; haemostatic; cell proliferation; immune disorder;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
 KW myasthenia gravis; systemic lupus erythematosus; SLE; diabetes; asthma;
 KW ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis;
 KW viral infection.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX Peptide 1..31
 XX Protein 32..162
 XX Region 41..56 /label= Mature_zalphall_ligand
 XX Region 69..84 /label= Helix_A
 XX Region 92..105 /label= Helix_B
 XX Region 135..148 /label= Helix_C
 XX Region 136..138 /label= Helix_D
 XX Region 136..138 /note= "Conserved region"
 XX
 XX WO200177171-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 03-APR-2001; 2001WO-US010872.
 XX
 PR 05-APR-2000; 2000US-0194731P.
 XX
 PR 28-JUL-2000; 2000US-0222121P.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX

PI Sprecher CA, Novak JE, West JW, Presnell SR, Holly RD, Nelson AJ;
 XX WPI; 2002-025898/03.
 DR N-PSDB; AAD22923.
 XX
 XX Novel soluble receptor polypeptides and polynucleotides used as cytokine
 XX antagonist for stimulating ligand activity-induced proliferation of
 XX hematopoietic cells and for suppressing immune response in a mammal.
 XX
 XX Claim 1; Page 181; 243pp; English.
 XX
 XX The invention relates to an isolated soluble zalphall cytokine receptor
 XX polypeptide and their cDNA molecules. Zalpha proteins are useful for
 XX inhibiting or antagonising the ligand activity-induced proliferation of
 XX haematopoietic cells and haematopoietic cell progenitors preferably
 XX lymphoid cells which are natural killer cells or cytotoxic T cells.
 XX Zalpha is useful for treating immune and inflammatory disorders, for
 XX reducing proliferation of neoplastic B or T cells, for suppressing an
 XX immune response in a mammal exposed to an antigen or pathogen. Zalpha is
 XX useful for treating diseases that require immune regulation including
 XX autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
 XX myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes;
 XX asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease,
 XX sepsis, viral infection (dengue virus infection) and cancer. The present
 XX sequence is human soluble Zalphall cytokine receptor ligand
 XX
 XX Sequence 162 AA;
 XX

Query Match 100.0%; Score 850; DB 5; Length 162;
 Best Local Similarity 100.0%; Pred. No. 1.3e-86;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGNMERIVICLMVIFLGLTVHKSSQGGDRHMRQLIDVDQLKNYNDLVPEF 60
 DB 1 MRSSPGNMERIVICLMVIFLGLTVHKSSQGGDRHMRQLIDVDQLKNYNDLVPEF 60

QY 61 LPAPEDVETNCEWSAFSCFQKQALKSANTGNNERIINVSIKKLKRKPPSTNAGRQKHL 120
 DB 61 LPAPEDVETNCEWSAFSCFQKQALKSANTGNNERIINVSIKKLKRKPPSTNAGRQKHL 120

QY 121 TCPSCDSYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
 DB 121 TCPSCDSYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 3
 AAU11965
 ID AAU11965 standard; protein; 162 AA.
 XX
 AC AAU11965;
 DT 09-APR-2002 (first entry)
 XX
 XX Human zalphall ligand polypeptide.
 XX
 KW Cytokine; zalphall ligand; zalphall receptor; NK cell progenitor;
 KW natural killer cell proliferation; T-cell proliferation;
 KW B-cell proliferation; anti-tumour response; immune system;
 KW immunostimulant; cytostatic; human; hPBCS;
 KW activated human peripheral blood cell.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX Peptide 1..31
 XX Protein 32..162 /label= Signal_peptide
 XX /label= Mature_zalphall_ligand
 XX
 XX US6307024-B1.
 XX
 PD 23-OCT-2001.
 XX

PF 09-MAR-2000; 2000US-00522217.
XX 09-MAR-1999; 99US-0123547P.
PR 11-MAR-1999; 99US-0123904P.
PR 01-JUL-1999; 99US-0142013P.
XX (ZYMO) ZYMOGENETICS INC.
XX Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX WPI; 2002-040208/05.
DR N-PSDB; AAS20637.
XX New zalphall ligand polypeptides and polynucleotides, useful for
PT stimulating proliferation, activation, differentiation and/or induction
PT of inhibition of specialized cell function, or for stimulating an
PT antigenic response.
XX Claim 7; Col 125-126; 105pp; English.
XX The present invention relates to the isolation of a novel cytokine,
CC zalphall ligand and the polynucleotide encoding it. The invention also
CC gives the sequence for the zalphall receptor and the polynucleotide
CC encoding it. The zalphall ligand polypeptide stimulates proliferation of
CC natural killer (NK) cells or NK cell progenitors, the activation of NK
CC cells, proliferation of T-cells, proliferation of B-cells stimulated with
CC anti-CD40 antibodies, stimulates an antigenic response in a mammal, and
CC reduces proliferation of B-cells stimulated with anti-1Gm antibodies. The
CC zalphall ligand polypeptide is also useful in preparing antibodies that
CC bind to zalphall ligand epitopes. The zalphall ligand polynucleotides can
CC be used as probes or primers to clone regions of a zalphall ligand gene,
CC and in gene therapy. Zalphall ligand may also be used to identify
CC inhibitors of its activity, to enhance the generation of anti-tumour
CC responses with or without the infusion of donor lymphocytes, and to
CC activate or stimulate the immune system. The present sequence represents
CC human zalphall ligand polypeptide. The cDNA encoding this is isolated
CC from a cDNA library from activated human peripheral blood cells (hPBGS)
XX
XX Sequence 162 AA;
XX
XX Query Match 100.0%; Score 850; DB 5; Length 162;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-86;
XX Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRSSPGNMERIVICLVIFLGTIVHKSSSGQDRHMRQLIDIVDQKYNVDLVPF 60
DB 1 MRSSPGNMERIVICLVIFLGTIVHKSSSGQDRHMRQLIDIVDQKYNVDLVPF 60
QY 61 LPAPEDVETNCWSAFSCFQKALKSANTGNNERIINVSIKLKRKPPSTNAGRQKHL 120
DB 61 LPAPEDVETNCWSAFSCFQKALKSANTGNNERIINVSIKLKRKPPSTNAGRQKHL 120
QY 121 TPCSDSYKKPKPKFLEPKSLLOKWIHOHLSSRTHGSEDS 162
DB 121 TPCSDSYKKPKPKFLEPKSLLOKWIHOHLSSRTHGSEDS 162
RESULT 4
ABR61407
ID ABR61407 standard; protein; 162 AA.
XX
XX ABR61407;
XX
XX 12-AUG-2003 (first entry)
DT Human IL-21 SEQ ID NO:19.
DE
XX
XX arthritic disorder; interleukin-21; IL-21; IL-21 receptor; IL-21R;
XX immune cell activity; cancer; infectious disorder; antirheumatic;
XX antiarthritic; osteoparastic; antipsoriatic; cytostatic; antibacterial;
XX virucide; antiparasitic; immunosuppressive; antidiabetic; dermatological;
XX neuroprotective; antiulcer; antiallergic; antianaemic; hepatotropic;
XX
KW antithyroid; antinflammatory; immune response; immune disorder;
KW autoimmune disease; human.
OS Homo sapiens.
XX WO2003028630-A2.
XX 10-APR-2003.
XX 04-OCT-2002; 2002WO-US029839.
XX 04-OCT-2001; 2001US-00972218.
PR 17-APR-2002; 2002US-0373746P.
XX (AMHP) WYETH.
XX Carter L, Whitters MJ, Collins M, Young DA, Larsen G;
PI Donaldson DD, Lowe LD, Dunnesi K, Ma M, Witek JS, Kasaian MT;
PI Ungar M;
XX WPI; 2003-430146/40.
DR N-PSDB; ACC80873.
XX Treating or preventing arthritic disorder, cancer or infectious disorders
PT in a subject, involves administering a modulator of interleukin-21 or its
PT receptor which modulate immune cell activity.
XX Disclosure; Page 37; 176pp; English.
XX The invention relates to a novel method for treating or preventing an
CC arthritic disorder in a subject. The method involves administering to the
CC subject an interleukin-21 (IL-21)/IL-21 receptor (IL-21R) antagonist
CC optionally in combination with another therapeutic agent, to inhibit or
CC reduce immune cell activity in the subject. The method is also useful for
CC treating or preventing cancer or an infectious disorder, in a subject, by
CC administering IL-21/IL-21R agonist, to increase immune cell activity. The
CC method of the invention has antirheumatic, antiarthritic, osteoparastic,
CC antipsoriatic, cytostatic, antibacterial, virucide, antiparasitic,
CC immunosuppressive, antidiabetic, neuroprotective, dermatological,
CC antiulcer, antiasthmatic, antiallergic, antianaemic, hepatotropic,
CC antithyroid, and antinflammatory activity. The method is useful for
CC treating or preventing an arthritic disorder such as rheumatoid
CC arthritis, juvenile rheumatoid arthritis, osteoarthritis, psoriatic
CC arthritis or ankylosing spondylitis, and also cancer such as solid
CC tumour, soft tissue tumour or metastatic lesion, or an infectious
CC disorder such as bacterial, viral or parasitic infection in a mammal,
CC preferably human. A method of the invention is also useful for
CC increasing the ability of a vaccine composition containing an antigen to
CC elicit a protective immune response in a subject against the antigens.
CC The antigen is from a pathogen such as virus, bacterium or protozoan, or
CC from cancer or tumour cell antigen, or expressed on the surface of cancer
CC cell. An alternative method of the invention is useful for modulating the
CC activity of immune or haematopoietic cells and thus to treat or prevent a
CC variety of immune disorders, such as autoimmune diseases, for example
CC diabetes mellitus, multiple sclerosis, myasthenia gravis, systemic lupus
CC erythematosus, dermatitis, ulcer, asthma, allergic asthma, anaemia,
CC hepatitis, Graves's disease, graft versus host disease, and scleroderma.
CC The present sequence is used in an exemplification of the invention
XX
XX Sequence 162 AA;
XX
XX Query Match 100.0%; Score 850; DB 6; Length 162;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-86;
XX Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRSSPGNMERIVICLVIFLGTIVHKSSSGQDRHMRQLIDIVDQKYNVDLVPF 60
DB 1 MRSSPGNMERIVICLVIFLGTIVHKSSSGQDRHMRQLIDIVDQKYNVDLVPF 60
QY 61 LPAPEDVETNCWSAFSCFQKALKSANTGNNERIINVSIKLKRKPPSTNAGRQKHL 120
DB 61 LPAPEDVETNCWSAFSCFQKALKSANTGNNERIINVSIKLKRKPPSTNAGRQKHL 120

QY 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162
 Db 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162

RESULT 5

AAE14932
 ID AAE14932 standard; protein; 162 AA.

AC AAE14932;

XX 27-AUG-2003 (first entry)

XX Human interleukin-21 (IL-21).

XX Interleukin-21; IL-21; antagonist; cancer; inflammatory;
 KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
 KW systemic lupus erythematosus; myasthenia gravis; diabetes; human;
 KW zalphall ligand.
 XX OS Homo sapiens.

XX Key Location/Qualifiers

FT Region 41..56

FT /label= Helix_A

FT Binding-site 44

FT /note= "Important for IL-21 binding to its receptor"

FT Binding-site 47

FT /note= "Important for IL-21 binding to its receptor"

FT Region 57..68

FT /label= A/B_loop

FT Region 69..84

FT /label= Helix_B

FT Region 85..91

FT /label= B/C_loop

FT Region 92..105

FT /label= Helix_C

FT Region 106..134

FT /label= C/D_loop

FT Region 135..148

FT /label= Helix_D

FT Binding-site 135

FT /note= "Important for IL-21 binding to its receptor"

XX WO2003040313-A2.

XX 15-MAY-2003.

XX 28-OCT-2002; 2002WO-US034502.

XX 05-NOV-2001; 2001US-0337586P.

XX (ZYMO) ZYMOGENETICS INC.

XX Presnell SR, West JW, Novak JE;

XX WPI; 2003-441547/41.

XX N-PSDB; RAD47852.

XX New IL-21 polypeptide and encoding polynucleotide, useful for diagnosing

XX and treating disorders with aberrant expression or activity of the IL-21
 XX polypeptide, such as cancer, rheumatoid arthritis, multiple sclerosis and
 XX diabetes.
 XX Disclosure; Page 53-54; 71pp; English.

XX The invention relates to polynucleotides and polypeptides of interleukin-

XX 21 (IL-21) antagonists, that bind with specificity and exhibit an EC50
 XX that is not detectable in receptor binding studies. The antagonists of
 XX the invention have mutations in the D helix of the IL-21 molecule, and
 XX can be used to inhibit the activity of IL-21 with its cognate receptor.
 XX The IL-21 antagonists are useful for diagnosing and treating disorders
 XX involving the aberrant expression or activity of the IL-21 polypeptide,

CC such as cancer, inflammatory and autoimmune disorders, including
 CC rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,
 CC myasthenia gravis and diabetes. The polypeptides can also be used to
 CC prepare antibodies that bind IL-21 epitopes, peptides or polypeptides,
 CC and for enhancing in vivo killing of target tissues. The present sequence
 CC is human IL-21 (originally designated zalphall ligand)

XX SQ Sequence 162 AA;

Query Match 100.0%; Score 850; DB 7; Length 162;

Best lcal Similarity 100.0%; Pred. No. 1.3e-86;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSPGNMERIVICLWIFLGLTVHKSSSQGDHMRMRQLDIVDOLKXVNDLVPEF 60

Db 1 MRSPGNMERIVICLWIFLGLTVHKSSSQGDHMRMRQLDIVDOLKXVNDLVPEF 60

QY 61 LPAPEDVETNCSEAFSCFQKAQIKSANTGNRRRIINVSICKKRRKPPSTNAGRQKRL 120

Db 61 LPAPEDVETNCSEAFSCFQKAQIKSANTGNRRRIINVSICKKRRKPPSTNAGRQKRL 120

QY 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162

Db 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162

RESULT 6

ABU62893

ID ABU62893 standard; protein; 162 AA.

XX AC ABU62893;

XX 15-SEP-2003 (first entry)

XX Human interleukin 21 (IL-21).

XX Human; MU-1; haematopoietin receptor superfamily chain; immunomodulator;
 XX cytostatic; antibacterial; virucide; antianaemic; gene therapy;
 XX haematopoiesis; anaemias; immune response; cancer; infection;
 XX transplanted organ; cytokine; receptor; interleukin 21; IL21.
 XX Homo sapiens.

XX US2003049798-A1

XX 13-MAR-2003.

XX 04-OCT-2001; 2001US-00972218.

XX 17-MAR-1998; 98US-00040005.

XX 28-APR-2000; 2000US-00560766.

XX 11-MAY-2000; 2000US-00569384.

XX (CART/) CARTER L.

XX (WHIT/) WHITTERS M J.

XX (COLL/) COLLINS M.

XX (YOUNG/) YOUNG D A.

XX (DONA/) DONALDSON D D.

XX (LOWE/) LOWE L D.

XX (UNGE/) UNGER M.

XX Carter L, Whitters MJ, Collins M, Young DA, Donaldson DD;

XX Lowe LD, Unger M;

XX WPI; 2003-512354/48.

XX N-PSDB; ACD26729.

XX New fusion polypeptide for regulating hematopoiesis and immune responses,

XX comprises a fragment of a MU-1 polypeptide and a non-MU-1 fusion

XX polypeptide.

XX Disclosure; Page 10; 26pp; English.

CC The invention describes a fusion polypeptide comprising at least a
 CC fragment of a MU-1 polypeptide and a non-MU-1 fusion polypeptide. The
 CC polypeptide is useful in regulating haematopoiesis (e.g. in cases of
 CC anaemias) and/or immune responses (e.g. immune response to cancer,
 CC infections or to a transplanted organ) and in identifying other members
 CC of the haematopoietin superfamily, including cytokines and receptors. The
 CC polynucleotide may be used to express recombinant protein for analysis,
 CC characterisation or therapeutic use; and as markers for tissues or
 CC chromosomes. The polypeptide and polynucleotide may also be used as
 CC nutritional sources or supplements. This is the amino acid sequence of
 CC human interleukin 21 (IL21), a cytokine receptor that can be used to
 CC characterise the novel haematopoietin receptor of the invention
 XX
 XX Sequence 162 AA;

Query Match 100.0%; Score 850; DB 7; Length 162;
 Best Local Similarity 100.0%; Pred. No. 1.3e-86;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRSSPGNMERIVICLMVIFGLTVHKSSQGDHMRMRQLIDVDQLKNYVNDLVPEF 60
 DB 1 MRSSPGNMERIVICLMVIFGLTVHKSSQGDHMRMRQLIDVDQLKNYVNDLVPEF 60
 QY 61 LPAPEDVETNCEWSAFSCFQKALXSANTGNNRIINVSIIKKLKKPPSTNAGRQKHRL 120
 DB 61 LPAPEDVETNCEWSAFSCFQKALXSANTGNNRIINVSIIKKLKKPPSTNAGRQKHRL 120
 QY 121 TCPSCDSYKPKPKFLERFKSLQKMIHQHLSRTHGSEDS 162
 DB 121 TCPSCDSYKPKPKFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 7
 ADE85808
 ID ADE85808 standard; protein; 162 AA.
 XX
 AC ADE85808;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human interleukin-21.
 XX
 KW Human; interleukin-21; immunosuppressive; antirheumatic; antiarthritic;
 KW antinflammatory; dermatological; ophthalmological; uropathic;
 KW muscular-gen.; vasotropic; antidiabetic; antithyroid; thyromimetic;
 KW neuroprotective; gastrointestinal-gen.; antipsoriatic; gene therapy.
 OS Homo sapiens.
 XX
 PN WO2003087320-A2.
 XX
 PD 23-OCT-2003.
 XX
 PF 08-APR-2003; 2003WO-US010736.
 XX
 PR 09-APR-2002; 2002US-0371038P.
 XX
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 XX
 PI Moll T, Strom TB, Zheng XX;
 XX
 DR WPI; 2003-845317/78.
 XX

PT New substantially pure interleukin-21 polypeptide, useful for diagnosing,
 PT treating and prognosticating autoimmune disorders, e.g. rheumatic
 PT disease, type I diabetes, Graves disease, multiple sclerosis, psoriasis
 PT and myasthenia gravis.
 XX

PS Disclosure; SEQ ID NO 1; 65pp; English.

XX
 CC The present sequence is the protein sequence of human interleukin-21 (IL-
 CC 21). The invention provides antagonists of the IL-21 receptor. These
 CC include mutants of murine IL-21 in which the Gln residue at position 119

CC of the mature polypeptide is substituted by Asp or in which the Gln
 CC residues at positions 114 and 119 of the mature polypeptide are both
 CC replaced by Asp. The mutant IL-21 polypeptides inhibit or suppress T-cell
 CC activation. They preferably comprise a sequence that increases
 CC circulating half-life, such as the Fc region of an IgG molecule and may
 CC further comprise an antigenic tag. Such antagonists inhibit cellular
 CC proliferation in response to either anti-CD3 monoclonal antibodies or
 CC anti-CD3 antibodies applied together with IL-2 and/or IL-15 together with
 CC IL-21. A claimed method of suppressing the immune response in a patient
 CC comprises administering the IL-21 antagonist or a nucleic acid encoding
 CC it. The method is used to treat an autoimmune disease such as rheumatic
 CC disease, including systemic lupus erythematosus, Sjogren's syndrome,
 CC scleroderma, mixed connective tissue disease, dermatomyositis,
 CC polymyositis, Reiter's syndrome, or Behcet's disease, or rheumatoid
 CC arthritis, type I diabetes, autoimmune disease of the thyroid such as
 CC Hashimoto's thyroiditis or Graves' disease, an autoimmune disease of the
 CC central nervous system such as multiple sclerosis, myasthenia gravis, or
 CC encephalomyelitis, or an autoimmune disease selected from pemphigus
 CC vulgaris, pemphigus vegetans, pemphigus foliaceus, Seneear-Usher syndrome,
 CC Brazilian pemphigus, psoriasis or inflammatory bowel disease (all
 CC claimed).

XX Sequence 162 AA;

Query Match 100.0%; Score 850; DB 7; Length 162;
 Best Local Similarity 100.0%; Pred. No. 1.3e-86;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRSSPGNMERIVICLMVIFGLTVHKSSQGDHMRMRQLIDVDQLKNYVNDLVPEF 60
 DB 1 MRSSPGNMERIVICLMVIFGLTVHKSSQGDHMRMRQLIDVDQLKNYVNDLVPEF 60
 QY 61 LPAPEDVETNCEWSAFSCFQKALXSANTGNNRIINVSIIKKLKKPPSTNAGRQKHRL 120
 DB 61 LPAPEDVETNCEWSAFSCFQKALXSANTGNNRIINVSIIKKLKKPPSTNAGRQKHRL 120
 QY 121 TCPSCDSYKPKPKFLERFKSLQKMIHQHLSRTHGSEDS 162
 DB 121 TCPSCDSYKPKPKFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 8
 AAE14934
 ID AAE14934 standard; protein; 162 AA.
 XX
 AC AAE14934;
 XX
 DT 27-AUG-2003 (first entry)
 XX
 DE Human interleukin-21 (IL-21) antagonist #2.
 XX
 KW Interleukin-21; IL-21; antagonist; cancer; inflammatory;
 KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
 KW systemic lupus erythematosus; myasthenia gravis; diabetes; human;
 KW zalphall ligand; mutant; mutein.

OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 145 /note= "Wild-type Gln substituted with Asp"
 FT FT
 FT Misc-difference 148 /note= "Wild-type Ile substituted with Asp"
 FT FT
 XX WO2003040313-A2.
 XX
 XX 15-MAY-2003.
 XX

XX 28-OCT-2002; 2002WO-US034502.

XX 05-NOV-2001; 2001US-0337586P.

XX

(ZYMO) ZYMOGENETICS INC.

Presnell SR, West JW, Novak JE;

WPI; 2003-441547/41.

N-PSDB; AAD47854.

New IL-21 polypeptide and encoding polynucleotide, useful for diagnosing PT and treating disorders with aberrant expression or activity of the IL-21 PT polypeptide, such as cancer, rheumatoid arthritis, multiple sclerosis and diabetes.

Claim 3; Page 58; 71pp; English.

The invention relates to polynucleotides and polypeptides of interleukin-21 (IL-21) antagonists, that bind with specificity and exhibit an EC50 that is not detectable in receptor binding studies. The antagonists of the invention have mutations in the D helix of the IL-21 molecule, and can be used to inhibit the activity of IL-21 with its cognate receptor. The IL-21 antagonists are useful for diagnosing and treating disorders involving the aberrant expression or activity of the IL-21 polypeptide, such as cancer, inflammatory and autoimmune disorders, including rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus, myasthenia gravis and diabetes. The polypeptides can also be used to prepare antibodies that bind IL-21 epitopes, peptides or polypeptides, and for enhancing in vivo killing of target tissues. The present sequence is human IL-21 antagonist. The antagonist molecule is a mutant of IL-21 polypeptide, with Gln145Asp and Ile148Asp substitutions. The resulting mutant was designated zalphall ligand Q153D/1156D

Sequence 162 AA;

Query Match 97.8%; Score 831; DB 7; Length 162;

Best Local Similarity 98.1%; Pred. No. 1.7e-84;
Matches 159; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRSPGNMERIVICLMVIFGLTVHKSSSQQRHMRMQQLDIVDQKKNYVNDLVPEF 60
DB 1 MDSPFGNMERIVICLMVIFGLTVHKSSSQQRHMRMQQLDIVDQKKNYVNDLVPEF 60
QY 61 LPAPEDVETNCWEAFSCFQKQAKLSANTGNRRIINVSIKLKRKPPSTNAGRQKHRL 120
DB 61 LPAPEDVETNCWEAFSCFQKQAKLSANTGNRRIINVSIKLKRKPPSTNAGRQKHRL 120
QY 121 TCPSCDSYEKKPKPEFLERFKSLLOKMHLSRTHGSEDS 162
DB 121 TCPSCDSYEKKPKPEFLERFKSLLDKMDHQLSRTHGSEDS 162

RESULT 9

AAE14933

ID AAE14933 standard; protein; 147 AA.

AC AAE14933;

DT 27-AUG-2003 (first entry)

Human interleukin-21 (IL-21) antagonist #1.

Interleukin-21; IL-21; antagonist; cancer; inflammatory;
autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
systemic lupus erythematosus; myasthenia gravis; diabetes; human;
zalphall ligand; mutant; mutein.

Homo sapiens.

Synthetic.

Key Location/Qualifiers

Misc-difference 145

/note= "Wild-type Gln substituted with Asp"

WO2003040313-A2.

15-MAY-2003.

28-OCT-2002; 2002WO-US034502.

05-NOV-2001; 2001US-0337586P.

(ZYMO) ZYMOGENETICS INC.

Presnell SR, West JW, Novak JE;

WPI; 2003-441547/41.

N-PSDB; AAD47853.

New IL-21 polypeptide and encoding polynucleotide, useful for diagnosing PT and treating disorders with aberrant expression or activity of the IL-21 PT polypeptide, such as cancer, rheumatoid arthritis, multiple sclerosis and diabetes.

Claim 3; Page 55-56; 71pp; English.

The invention relates to polynucleotides and polypeptides of interleukin-21 (IL-21) antagonists, that bind with specificity and exhibit an EC50 that is not detectable in receptor binding studies. The antagonists of the invention have mutations in the D helix of the IL-21 molecule, and can be used to inhibit the activity of IL-21 with its cognate receptor. The IL-21 antagonists are useful for diagnosing and treating disorders involving the aberrant expression or activity of the IL-21 polypeptide, such as cancer, inflammatory and autoimmune disorders, including rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus, myasthenia gravis and diabetes. The polypeptides can also be used to prepare antibodies that bind IL-21 epitopes, peptides or polypeptides, and for enhancing in vivo killing of target tissues. The present sequence is human IL-21 antagonist. The antagonist molecule is a mutant of IL-21 polypeptide, with truncation after residue 147 (Met) and Gln145Asp substitution. The resulting mutant was designated zalphall ligand I156ST/Q153D

Sequence 147 AA;

Query Match 89.2%; Score 758; DB 7; Length 147;

Best Local Similarity 98.6%; Pred. No. 2.2e-76;
Matches 145; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRSPGNMERIVICLMVIFGLTVHKSSSQQRHMRMQQLDIVDQKKNYVNDLVPEF 60
DB 1 MDSPFGNMERIVICLMVIFGLTVHKSSSQQRHMRMQQLDIVDQKKNYVNDLVPEF 60
QY 61 LPAPEDVETNCWEAFSCFQKQAKLSANTGNRRIINVSIKLKRKPPSTNAGRQKHRL 120
DB 61 LPAPEDVETNCWEAFSCFQKQAKLSANTGNRRIINVSIKLKRKPPSTNAGRQKHRL 120
QY 121 TCPSCDSYEKKPKPEFLERFKSLLOKMHLSRTHGSEDS 147
DB 121 TCPSCDSYEKKPKPEFLERFKSLLDKMHLSRTHGSEDS 147

RESULT 10

AAB18627

ID AAB18627 standard; protein; 519 AA.

AC AAB18627;

DT 22-JAN-2001 (first entry)

Amino acid sequence of MBP-human zalphall ligand fusion in pTAP126.

zalphall ligand; cytokine; haematopoietic cell proliferation; lymphoma;
tumorigenesis; leukaemia; hematopoiesis; B cell tumour.

Synthetic.

Homo sapiens.

WO200053761-A2.

```

XX 14-SEP-2000.
PD
PF
XX 09-MAR-2000; 2000WC-US006067.
XX
XX 09-MAR-1999; 99US-00264908.
XX
XX 11-MAR-1999; 99US-00265992.
XX
XX 01-JUL-1999; 99US-0142013P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
XX Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
XX WPI: 2000-565600/52.
XX N-PSDB; AAB75599.
XX
XX New human cytokine, designated zalphall ligand, useful for stimulating
XX the proliferation and/or development of hematopoietic cells in vitro and
XX in vivo, and for treating tumorigenesis.
XX
XX Example 31; Page 233-235; 256pp; English.
XX
XX The present sequence represents a MBP-human zalphall ligand fusion in the
XX plasmid pTAP126. Zalphall ligand is a cytokine. The zalphall ligand is
XX useful for stimulating the proliferation and development of
XX haematopoietic cells in vitro and in vivo. Zalphall ligand
XX polynucleotides can be used as primers or probes for cloning the zalphall
XX gene. The zalphall ligand is useful for treating tumorigenesis. A
XX zalphall ligand-saporin fusion toxin may be used for treating leukaemias
XX and lymphomas. Antagonists against zalphall ligand are useful as research
XX reagents for characterizing ligand-receptor interaction. Antagonists are
XX also useful for inhibiting expansion, proliferation, activation and
XX differentiation of cells involved in regulating hematopoiesis. The
XX zalphall ligand may also be used to stimulate an immune response against
XX B cell tumour, a virus, a parasite or a bacterium. The zalphall
XX polypeptides, polynucleotides, antagonists, agonists and antibodies are
XX also useful for the detection, diagnosis, prevention, and treatment of
XX diseases associated with a zalphall ligand genetic defect
XX
XX Sequence 519 AA;
XX
XX Query Match 81.8%; Score 695.5; DB 3; Length 519;
XX Best Local Similarity 95.7%; Pred. No. 1.1e-68;
XX Matches 134; Conservative 1; Mismatches 2; Indels 3; Gaps 1;
XX
XX 23 LVHKSSSQGDHMTMRQLIDVDQKNYVNDLVPEFLPAPEDVETNCWSAFSCFQKA 82
XX 383 LVPRGS---QDRHMTMRQLIDVDQKNYVNDLVPEFLPAPEDVETNCWSAFSCFQKA 439
XX
XX 83 QLKSAANTGNNERIINVSIXKLKRPSTNAGRQKRLTQPCSDSYEKPKPFLEFRPKS 142
XX 440 QLKSAANTGNNERIINVSIXKLKRPSTNAGRQKRLTQPCSDSYEKPKPFLEFRPKS 499
XX
XX 143 LQKMIHQHLSRTHGSEDS 162
XX 500 LQKMIHQHLSRTHGSEDS 519
XX
XX RESULT 11
XX AAU11971
XX
XX ID AAU11971 standard; protein; 519 AA.
XX
XX AC AAU11971;
XX
XX 09-APR-2002 (first entry)
XX
XX MBP-human zalphall Ligand fusion protein.
XX
XX Cytokine; zalphall Ligand; zalphall receptor; NK cell progenitor;
XX natural killer cell proliferation; T-cell proliferation; mutant;
XX B-cell proliferation; anti-tumour response; immune system; MBP;
XX immunostimulant; cytostatic; human; maltose binding protein; mutin.

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XX Homo sapiens.
XX OS Synthetic.
XX
XX PN US6307024-B1.
XX
XX PD 23-OCT-2001.
XX
XX PF 09-MAR-2000; 2000US-00522217.
XX
XX PR 09-MAR-1999; 99US-0123547P.
XX 11-MAR-1999; 99US-0123904P.
XX PR 01-JUL-1999; 99US-0142013P.
XX
XX FA (ZYMO ) ZYMOGENETICS INC.
XX
XX PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
XX PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
XX DR WPI: 2002-040208/05.
XX DR N-PSDB; AAS20714.
XX
XX PT New zalphall ligand polypeptides and polynucleotides, useful for
XX stimulating proliferation, activation, differentiation and/or induction
XX of/inhibition of specialized cell function, or for stimulating an
XX antigenic response.
XX
XX PS Example 31; Col 161-166; 105pp; English.
XX
XX CC The present invention relates to the isolation of a novel cytokine,
XX zalphall Ligand and the polynucleotide encoding it. The invention also
XX gives the sequence for the zalphall receptor and the polynucleotide
XX encoding it. The zalphall Ligand polypeptide stimulates proliferation of
XX natural killer (NK) cells or NK cell progenitors, the activation of NK
XX cells, proliferation of T-cells, proliferation of B-cells stimulated with
XX anti-CD40 antibodies, stimulates an antigenic response in a mammal, and
XX reduces proliferation of B-cells stimulated with anti-IGM antibodies. The
XX zalphall Ligand polypeptide is also useful in preparing antibodies that
XX bind to zalphall Ligand epitopes. The zalphall Ligand polynucleotides can
XX be used as probes or primers to clone regions of a zalphall Ligand gene,
XX and in gene therapy. Zalphall Ligand may also be used to identify
XX inhibitors of its activity, to enhance the generation of anti-tumour
XX responses with or without the infusion of donor lymphocytes, and to
XX activate or stimulate the immune system. The present sequence
XX representing MBP-human zalphall Ligand fusion protein is used in the
XX methods of the present invention
XX
XX SQ Sequence 519 AA;
XX
XX Query Match 81.8%; Score 695.5; DB 5; Length 519;
XX Best Local Similarity 95.7%; Pred. No. 1.1e-68;
XX Matches 134; Conservative 1; Mismatches 2; Indels 3; Gaps 1;
XX
XX QY 23 LVHKSSSQGDHMTMRQLIDVDQKNYVNDLVPEFLPAPEDVETNCWSAFSCFQKA 82
XX 383 LVPRGS---QDRHMTMRQLIDVDQKNYVNDLVPEFLPAPEDVETNCWSAFSCFQKA 439
XX
XX QY 83 QLKSAANTGNNERIINVSIXKLKRPSTNAGRQKRLTQPCSDSYEKPKPFLEFRPKS 142
XX 440 QLKSAANTGNNERIINVSIXKLKRPSTNAGRQKRLTQPCSDSYEKPKPFLEFRPKS 499
XX
XX QY 143 LQKMIHQHLSRTHGSEDS 162
XX 500 LQKMIHQHLSRTHGSEDS 519
XX
XX RESULT 12
XX AAB18624
XX ID AAB18624 standard; protein; 146 AA.
XX
XX AC AAB18624;
XX
XX DT 22-JAN-2001 (first entry)

```

XX DE A mouse zalphall ligand polypeptide.
 XX DE zalphall ligand, cytokine, haematopoietic cell proliferation; lymphoma;
 KW tumorigenesis; leukaemia; haematopoiesis; B cell tumour.
 XX OS Mus musculus.
 XX PN WO200053761-A2.
 XX PD 14-SEP-2000.
 XX PF 09-MAR-2000; 2000WO-US006067.
 XX PR 09-MAR-1999; 99US-00264908.
 XX PR 11-MAR-1999; 99US-00265992.
 XX PR 01-JUL-1999; 99US-0142013P.
 XX PA (Zymo) ZYMOGENETICS INC.
 XX PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
 XX PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
 XX DR WPI: 2000-565600/52.
 XX DR N-PSDB; AAA75580.
 XX PT New human cytokine, designated zalphall ligand, useful for stimulating
 XX PT the proliferation and/or development of hematopoietic cells in vitro and
 XX PT in vivo, and for treating tumorigenesis.
 XX PS Disclosure; Page 222-223; 256pp; English.
 XX CC The present sequence represents a mouse zalphall ligand polypeptide,
 XX CC which is a cytokine. The zalphall ligand is useful for stimulating the
 XX CC proliferation and development of haematopoietic cells in vitro and in
 XX CC vivo. Zalphall ligand polynucleotides can be used as primers or probes
 XX CC for cloning the zalphall gene. The zalphall ligand is useful for treating
 XX CC tumorigenesis. A zalphall ligand-epoetin fusion toxin may be used for
 XX CC treating leukaemias and lymphomas. Antagonists against zalphall ligand
 XX CC are useful as research reagents for characterizing ligand-receptor
 XX CC interaction. Antagonists are also useful for inhibiting expansion,
 XX CC proliferation, activation and differentiation of cells involved in
 XX CC regulating haematopoiesis. The zalphall ligand may also be used to
 XX CC stimulate an immune response against B cell tumour, a virus, a parasite
 XX CC or a bacterium. The zalphall polypeptides, polynucleotides, antagonists,
 XX CC agonists and antibodies are also useful for the detection, diagnosis,
 XX CC prevention, and treatment of diseases associated with a zalphall ligand
 XX CC genetic defect
 XX CC Sequence 146 AA;
 XX SQ

Query Match 57.2%; Score 486; DB 3; Length 146;
 Best Local Similarity 63.0%; Pred. No. 5.6e-46;
 Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;
 Oy 8 MERIVICLVIFLGTVAHSSQODRHMRMRLIDIVDLQKNYNDLVPEFLPAPEDV 67
 Db 1 MERTLVCLVIFLGTVAHSSQODRHMRMRLIDIVDLQKNYNDLVPEFLPAPEDV 60
 Oy 68 ETNCEWSAFSCFQAKLKSANTGNRIINVSICKLRKPPSTNAGRQKHRLTSPSCDS 127
 Db 61 KGHCEHAFAFCQAKLKPSNPGNKTFFIDLVAQLRRRLPARRGGKKQKHIAKCPSCDS 120
 Oy 128 YEKKPPKEFLERFKSLQKMIHQHLS 153
 Db 121 YEKTPKEFLERLKLWLLQKMIHQHLS 146

RESULT 13
 AA013737
 ID AA013737 standard; protein; 146 AA.
 XX AC AA013737;

XX DT 26-FEB-2002 (first entry)
 XX DE Murine soluble Zalphall cytokine receptor ligand.
 XX KW Murine; Zalphall; cytokine receptor; immunosuppressive; cytostatic;
 XX KW inflammatory disorder; haemostatic; cell proliferation; immune disorder;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
 KW myasthenia gravis; systemic lupus erythematosus; SLE; diabetes; asthma;
 KW ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis;
 KW viral infection.
 XX OS Mus musculus.
 XX PN WO200177171-A2.
 XX PD 18-OCT-2001.
 XX PF 03-APR-2001; 2001WO-US010872.
 XX PR 05-APR-2000; 2000US-0194731P.
 XX PR 28-JUL-2000; 2000US-0222121P.
 XX PA (Zymo) ZYMOGENETICS INC.
 XX PI Sprecher CA, Novak JE, West JW, Presnell SR, Holly RD, Nelson AJ;
 XX DR WPI: 2002-025898/03.
 XX DR N-PSDB; AAD22952.
 XX PT Novel soluble receptor polypeptides and polynucleotides used as cytokine
 XX PT antagonist for stimulating ligand activity-induced proliferation of
 XX PT hematopoietic cells and for suppressing immune response in a mammal.
 XX PS Claim 1; Page 212; 243pp; English.
 XX CC The invention relates to an isolated soluble zalphall cytokine receptor
 XX CC polypeptide and their cDNA molecules. Zalphall proteins are useful for
 XX CC inhibiting or antagonising the ligand activity-induced proliferation of
 XX CC haematopoietic cells and haematopoietic cell progenitors preferably
 XX CC lymphoid cells which are natural killer cells or cytotoxic T cells.
 XX CC Zalphall is useful for treating immune and inflammatory disorders, for
 XX CC reducing proliferation of neoplastic B or T cells, for suppressing an
 XX CC immune response in a mammal exposed to an antigen or pathogen. Zalphall is
 XX CC useful for treating diseases that require immune regulation including
 XX CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
 XX CC myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes;
 XX CC asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease,
 XX CC sepsis, viral infection (dengue virus infection) and cancer. The present
 XX CC sequence is murine soluble Zalphall cytokine receptor ligand
 XX CC Sequence 146 AA;
 XX SQ

Query Match 57.2%; Score 486; DB 5; Length 146;
 Best Local Similarity 63.0%; Pred. No. 5.6e-46;
 Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;
 Oy 8 MERIVICLVIFLGTVAHSSQODRHMRMRLIDIVDLQKNYNDLVPEFLPAPEDV 67
 Db 1 MERTLVCLVIFLGTVAHSSQODRHMRMRLIDIVDLQKNYNDLVPEFLPAPEDV 60
 Oy 68 ETNCEWSAFSCFQAKLKSANTGNRIINVSICKLRKPPSTNAGRQKHRLTSPSCDS 127
 Db 61 KGHCEHAFAFCQAKLKPSNPGNKTFFIDLVAQLRRRLPARRGGKKQKHIAKCPSCDS 120
 Oy 128 YEKKPPKEFLERFKSLQKMIHQHLS 153
 Db 121 YEKTPKEFLERLKLWLLQKMIHQHLS 146

RESULT 14
 AA011968
 ID AA011968 standard; protein; 146 AA.

